

STIC-Biotech/ChemLib

178944

mej

From: Chan, Christina
Sent: Tuesday, February 07, 2006 7:28 PM
To: Basi, Nirmal; STIC-Biotech/ChemLib
Subject: RE: Rush search for App. #: 10/083,168

Please ~~rush~~ Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

STIC/CHEN DIVISION

FEB - 8 2006

-----Original Message-----

From: Basi, Nirmal
Sent: Tuesday, February 07, 2006 7:27 PM
To: Chan, Christina
Subject: Rush search for App. #: 10/083,168

Thurman I am seeking approval for a RUSH sequence search for an amended case, as indicated below. If approved, could you please forward the search to STIC and cc a copy to me.

Examiner: Nirmal S. Basi
Art Unit 1646
Office: Remsen Building, Room 4D68
Mail Room: Remsen Building, room 4C70

Sequence search:

App. #: 10/083,168
Result format: Paper.

Title: ENDOGENOUS AND NON-ENDOGENOUS VERSIONS OF HUMAN G PROTEIN-
COUPLED RECEPTORS

Inventors: Liaw et al

Priority Date: 4/14/97
Please search:
i) SEQ ID NOS: 16, 84 and 85

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 2-13-06
Searcher Prep Time: _____
Online Time: _____

Type of Search _____
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Search issued, commercial and interference databases.

Thanks,
Nirmal S. Basi

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2006, 00:47:19 ; Search time 214.5 Seconds
(without alignments)
632.951 Million cell updates/sec

Title: US-10-083-168-16
Perfect score: 1614
Sequence: 1 MNGYNTCGSSDLTPPAIK.....AVAPRAKAKHSQDSLCVTLA 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980a:*
2: geneseqp1990a:*
3: geneseqp2000a:*
4: geneseqp2001a:*
5: geneseqp2002a:*
6: geneseqp2003a:*
7: geneseqp2003bs:*
8: geneseqp2004a:*
9: geneseqp2005a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1614	100.0	309	3 AAY79576	Aay79576 Human G p
2	1614	100.0	309	5 ABG95159	Abg95159 Human GPC
3	1614	100.0	309	6 ABP82002	Abp82002 Human G p
4	1614	100.0	309	7 ADB67656	Adb67656 Human G p
5	1614	100.0	309	8 ADO29394	Ado29394 Human GPC
6	1614	100.0	309	8 ADO78094	Ado78094 Human GPC
7	1614	100.0	309	9 ADV73203	Adv73203 Human col
8	1614	100.0	309	9 AEB15039	Aeb15039 Human GPC
9	1609	99.7	309	5 ABG95172	Abg95172 Human GPC
10	1608	99.6	309	3 AAY69989	Aay69989 Human rec
11	1608	99.6	547	7 ADF70461	Adf70461 Orphan re
12	1606	99.5	309	7 ADF50511	Adf50511 Human GPC
13	1602	99.3	309	3 AAY58645	Aay58645 Human G-p
14	1602	99.3	309	6 ADA84069	Ada84069 Human GPR
15	1602	99.3	394	8 ADO78095	Ado78095 Human GPR
16	1602	99.3	394	8 ADR10454	Adr10454 Human pro
17	1382	85.6	286	8 ADP29765	Adp29765 Human GPC
18	1124	69.6	307	8 ADO29395	Ado29395 Mouse GPC
19	402	24.9	370	2 AAW62597	Aaw62597 Human 7-t
20	402	24.9	370	5 ABP61511	Abp61511 Human NF-
21	402	24.9	370	6 ABG73513	Abg73513 Human p2y
22	402	24.9	370	6 ABP81870	Abp81870 Human G p
23	402	24.9	370	7 ADH69286	Adh69286 Human pur
24	402	24.9	370	8 ADF91778	Adf91778 Human P2Y

25	402	24.9	370	8 ADO29049	Ado29049 Human nov
26	402	24.9	370	8 ADQ88244	Adq88244 Human 241
27	402	24.9	370	8 ADQ81575	Adq81575 Human lys
28	402	24.9	370	8 ADS84260	Ads84260 Human G p
29	402	24.9	370	9 ADV35123	Adv35123 Human tra
30	402	24.9	608	7 ADF70491	Adf70491 Orphan re
31	401	24.8	370	7 ADH69285	Adh69285 Human pur
32	401	24.8	370	8 ADF91777	Adf91777 Human P2Y
33	397	24.6	370	8 ADO29050	Ado29050 Mouse nov
34	392	24.3	370	5 ABP61510	Abp61510 Human NF-
35	390	24.2	368	8 ADS84259	Ads84259 Human G p
36	385	23.9	327	8 ADO29415	Ado29415 Mouse GPC
37	381.5	23.6	363	9 ADW44804	Adw44804 Human RUP
38	381.5	23.6	363	9 AEB20962	Aeb20962 Human EPA
39	381.5	23.6	363	9 AEB20962	Adw44807 Human RUP
40	379.5	23.5	363	9 ADW44807	Adw44802 Human RUP
41	378.5	23.5	363	9 ADW44810	Adw44810 Human RUP
42	377.5	23.4	363	9 ADW44805	Adw44805 Human RUP
43	377.5	23.4	363	9 ADW44814	Adw44814 Human RUP
44	377.5	23.4	363	9 ADW44814	Adw44814 Human RUP
45	376.5	23.3	363	5 AAU77993	Aau77993 Human inf

ALIGNMENTS

RESULT 1
AAY79576
ID AAY79576 standard; protein; 309 AA.
XX AC AAY79576;
XX AC
DT 15-AUG-2000 (first entry)
XX
DE Human G protein coupled receptor GPR35.
XX
XX GPR35; G protein coupled receptor; human; NIDDM1;
KW non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10;
KW diagnosis; therapy.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 174
FT /note= "encoded by GCG"
FT Misc-difference 294
FT /note= "encoded by AGT"
XX
XX WO200023603-A2.
XX
XX 27-APR-2000.
XX
XX 21-OCT-1999; 99WO-US024890.
XX
XX 21-OCT-1998; 98US-0105052P.
XX 13-MAY-1999; 99US-0134175P.
XX
XX (ARCH-) ARCH DEV CORP.
XX (TEXA) UNIV OF TEXAS SYSTEM.
XX
XX Polonsky KS, Horikawa Y, Oda N, Sreenan S, Zhou Y, Otani K;
XX Hanis CL, Bell GI, Cox NJ;
XX
XX WPI; 2000-339702/29.
XX N-PSDB; AAA27485, AAY79574, AAY79576.
XX
XX Method for screening for type 2 diabetes mellitus comprises detecting a
XX polymorphism in a calpain encoding nucleic acid segment or a protease-
XX encoding nucleic acid segment.
XX
XX Claim 75; Page 237-238; 257pp; English.
XX
XX The present sequence is that of the human gene encoding G protein coupled

CC receptor, GPR35 as deduced from a composite cDNA (see AAA27485). The
 CC sequence of GPR35 is similar to that of a putative purinoceptor P2Y9
 CC (34.1% identity), suggesting that ATP or other nucleotides is its ligand.
 CC GPR35 mRNA was detected in all adult and foetal tissues examined with
 CC relatively higher levels in adult lung, small intestine, colon and
 CC stomach. In these tissues, there are 2 major transcripts of 2.4 and 4.4
 CC kb, whereas in skeletal muscle there is a single transcript of 9.4 kb.
 CC The GPR35 gene is located in a 49,136 bp region (see AAA27475) within the
 CC NIDDM1 region of human chromosome 2. This region also includes the CAPN10
 CC gene, which encodes a novel calpain-like cysteine protease, designated
 CC calpain 10. Mutations in the CAPN10 gene are responsible for
 CC susceptibility to type 2 diabetes. Claimed methods for screening for a
 CC propensity for type 2 diabetes mellitus are based on detection of a
 CC polymorphism in a calpain encoding nucleic acid. Methods are also claimed
 CC for identifying modulators of calpain activity, and using these
 CC modulators to treat diabetes, in particular through the regulation of an
 CC insulin secretory response or insulin mediated glucose transport
 CC
 CC Sequence 309 AA;

Query Match 100.0%; Score 1614; DB 3; Length 309;
 Best Local Similarity 100.0%; Pred. No. 3.1e-167;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPPAIKLGFYAVLVLGLLNSLALWVFCRMOQWTETRIYMT 60
 DB 1 MNGTYNTCGSSDLTPWPPAIKLGFYAVLVLGLLNSLALWVFCRMOQWTETRIYMT 60
 QY 61 NLAVADLCLLCTLPFVHLSDRTSDTPLCQLSQGIYLTNRYSISLVTIAVDVYAVRH 120
 DB 61 NLAVADLCLLCTLPFVHLSDRTSDTPLCQLSQGIYLTNRYSISLVTIAVDVYAVRH 120
 QY 121 PLRARGLSRQAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRTRHNFNSMRPPLG 180
 DB 121 PLRARGLSRQAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRTRHNFNSMRPPLG 180
 QY 181 YLPLAVVVFCSLKVTTALAQRPTDVGOAETRKARVMWANLLVFVVCFLPLHGLTVR 240
 DB 181 YLPLAVVVFCSLKVTTALAQRPTDVGOAETRKARVMWANLLVFVVCFLPLHGLTVR 240
 QY 241 LAVGNACALLETTIRRALYITTSKLSANCCCLDAICYTMMAKEFQASALAVAPRAKAHS 300
 DB 241 LAVGNACALLETTIRRALYITTSKLSANCCCLDAICYTMMAKEFQASALAVAPRAKAHS 300
 QY 301 QDSLCTVTLA 309
 DB 301 QDSLCTVTLA 309

RESULT 2

ABG95159
 ID ABG95159 standard; protein; 309 AA.

AC ABG95159;

XX 04-DEC-2002 (first entry)

XX Human GPCR GPR35.

XX Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;
 XX hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;
 XX psychotic disorder; asthma; bronchoespaem; anaesthesia;
 XX myocardial infarction; MI; stroke; glaucoma; anxiety;
 XX prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;
 XX prostatic hypertrophy; receptor.

XX Homo sapiens.

XX WO200268600-A2.

XX 06-SEP-2002.

XX 26-FEB-2002; 2002WO-US005625.

XX PR 26-FEB-2001; 2001US-0271913P.
 XX (AREN-) ARENA PHARM INC.
 XX Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;
 XX Lin I, Ortuno D;
 XX WPI; 2002-706980/76.
 XX N-PSDB; ABS73345.

PT New human G-protein coupled receptor (GPCR), useful for screening agonist
 or inverse agonist compounds for treating diseases associated with GPCR.

PS Claim 29; Page 128-130; 201pp; English.

XX The present invention relates to transmembrane receptors, particularly
 CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-
 CC endogenous) versions of the GPCRs, and the polynucleotide sequences
 CC encoding them. The GPCRs are useful for screening agonist or inverse
 CC agonist compounds for treating diseases associated with GPCR. Diseases
 CC that can be treated with such compounds include allergies, hypertension,
 CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic
 CC disorders, asthma, bronchoespaem, anaesthesia, myocardial infarction (MI),
 CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,
 CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present
 CC sequence represents an endogenous human GPCR

XX Sequence 309 AA;

Query Match 100.0%; Score 1614; DB 5; Length 309;
 Best Local Similarity 100.0%; Pred. No. 3.1e-167;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPPAIKLGFYAVLVLGLLNSLALWVFCRMOQWTETRIYMT 60
 DB 1 MNGTYNTCGSSDLTPWPPAIKLGFYAVLVLGLLNSLALWVFCRMOQWTETRIYMT 60
 QY 61 NLAVADLCLLCTLPFVHLSDRTSDTPLCQLSQGIYLTNRYSISLVTIAVDVYAVRH 120
 DB 61 NLAVADLCLLCTLPFVHLSDRTSDTPLCQLSQGIYLTNRYSISLVTIAVDVYAVRH 120
 QY 121 PLRARGLSRQAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRTRHNFNSMRPPLG 180
 DB 121 PLRARGLSRQAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRTRHNFNSMRPPLG 180
 QY 181 YLPLAVVVFCSLKVTTALAQRPTDVGOAETRKARVMWANLLVFVVCFLPLHGLTVR 240
 DB 181 YLPLAVVVFCSLKVTTALAQRPTDVGOAETRKARVMWANLLVFVVCFLPLHGLTVR 240
 QY 241 LAVGNACALLETTIRRALYITTSKLSANCCCLDAICYTMMAKEFQASALAVAPRAKAHS 300
 DB 241 LAVGNACALLETTIRRALYITTSKLSANCCCLDAICYTMMAKEFQASALAVAPRAKAHS 300
 QY 301 QDSLCTVTLA 309
 DB 301 QDSLCTVTLA 309

RESULT 3

ABP82002
 ID ABP82002 standard; protein; 309 AA.

XX AC ABP82002;

XX 04-MAR-2003 (first entry)

XX Human G protein-coupled receptor GPR35 protein SEQ ID NO:492.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 XX G protein-coupled receptor modulator; antibody; immune-related disease;
 XX growth-related disease; cell regeneration-related disease; AIDS; cancer;
 XX immunological-related cell proliferative disease; autoimmune disease;

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

OS Homo sapiens.

XX WO200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX N-PSDB; ABZ42852.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

XX Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, memory
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

XX Sequence 309 AA;

Query Match 100.0%; Score 1614; DB 6; Length 309;
Best Local Similarity 100.0%; Pred. No. 3.1e-167;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPAIKLGFYALVGLVLLVGLLNSLALVFCRQMQWTETRIYMT 60

Db 1 MNGTYNTCGSSDLTPWPAIKLGFYALVGLVLLVGLLNSLALVFCRQMQWTETRIYMT 60

QY 61 NLAVADCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTIAVDRYVAVRH 120

Db 61 NLAVADCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTIAVDRYVAVRH 120

QY 121 PLRAGLRSPRQAACAVLWLVIGSLVARWLLIGQGGFCFRSTRHNFSMRPPLLGF 180

Db 121 PLRAGLRSPRQAACAVLWLVIGSLVARWLLIGQGGFCFRSTRHNFSMRPPLLGF 180
QY 181 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKARVMWANLLVVFVCFPLPHVGLTVR 240
Db 181 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKARVMWANLLVVFVCFPLPHVGLTVR 240
QY 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKAHS 300
Db 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKAHS 300
QY 301 QDSLCLVTILA 309
Db 301 QDSLCLVTILA 309

RESULT 4

ADB67656

ID ADB67656 standard; protein; 309 AA.

XX ADB67656;

XX 04-DEC-2003 (first entry)

XX Human G protein-coupled receptor 35, SEQ ID 25.

XX Cardiant; Gene therapy; heart failure; human;

XX G protein-coupled receptor 35; receptor.

XX Homo sapiens.

XX WO2003072824-A1.

XX 04-SEP-2003.

XX 27-FEB-2003; 2003WO-JP0022228.

XX 28-FEB-2002; 2002JP-00054388.

XX 15-APR-2002; 2002JP-00112228.

XX (SANY) SANKYO CO LTD.

XX Kitakaze M, Takashima S, Asakura M, Isomura T, Furukawa H;

XX Koishi R, Nakamura K;

XX WPI; 2003-679959/64.

XX N-PSDB; ADB67672.

XX Predicting pathological conditions in heart failure using marker genes

XX and proteins.

XX Claim 1; Page 111-113; 137pp; Japanese.

XX The present invention relates to a method for predicting pathological

XX conditions in heart failure using expression of one of 17 gene sequences

XX (ADB67663-ADB67678); or protein sequences encoded by the genes (ADB67648-

XX ADB67662). The proteins and genes are useful for diagnosis, treatment and

XX prevention of heart failure.

XX Sequence 309 AA;

Query Match 100.0%; Score 1614; DB 7; Length 309;

Best Local Similarity 100.0%; Pred. No. 3.1e-167;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX DE Human GPR35 polypeptide.

XX KW G-protein coupled receptor 35; GPR35; G-protein coupled receptor; GPCR; screening; cardiovascular disease; gastrointestinal disease; liver disease; cancer; neoplasm; metabolic disorder; hematological disease; respiratory disease; inflammation; neurological disease; urological disorder; cardiovascular-gen.; gastrointestinal-gen.; hepatotropic; cytostatic; metabolic; antianemic; respiratory-gen.; antiinflammatory; neuroprotective; uterine; receptor.

XX OS Homo sapiens.

XX PN W02005059546-A2.

XX PD 30-JUN-2005.

XX PF 02-DEC-2004; 2004MO-EP013679.

XX PR 12-DEC-2003; 2003EP-00028614.

XX PA (FARB) BAYER HEALTHCARE AG.

XX PI Golz S, Brueggemeier U, Geerts A, Summer H;

XX PF WPI; 2005-506223/51.

XX DR N-PSDB; ABB15038.

XX PT Screening of therapeutic agents useful in treating specified diseases involves contacting test compound with G-protein coupled receptor GPR35, and detect binding of test compound to polypeptide.

XX PS Disclosure; SEQ ID NO 2; 96pp; English.

XX CC The invention relates to the use of human G-protein coupled receptor 35 (GPR35) for screening therapeutic agents useful in the treatment of cardiovascular disorders, liver and gastrointestinal diseases, cancer disorders, inflammatory diseases, metabolic diseases, hematological disorders, respiratory diseases, neurological disorders and urological disorders, in a mammal. GPR35 is a G-protein coupled receptor (GPCR). The therapeutic agents are screened by contacting a test compound with GPR35 polypeptide, and detecting the binding of the test compound to the polypeptide. Also described are: (1) a method of diagnosing the above specified diseases in a mammal, comprising determining the amount of a GPR35 polynucleotide in a sample taken from the mammal, and determining the amount of the GPR35 polynucleotide in healthy and/or diseased mammals; (2) a pharmaceutical composition for treating the above specified diseases in the mammal, comprising a therapeutic agent that binds to the GPR35 polypeptide; (3) use of regulators of a GPR35 for the preparation of the pharmaceutical composition or for the regulation of GPR35 activity in a mammal having the above specified diseases; and (4) a method for the preparation of the pharmaceutical composition, comprising identifying the GPR35 regulator, determining whether the regulator ameliorates the symptoms of the above specified diseases in a mammal, and combining the regulator with an acceptable pharmaceutical carrier. GPR35 is useful for screening therapeutic agents for treating cardiovascular disorders, liver and gastrointestinal diseases, cancer disorders, inflammatory diseases, metabolic diseases, hematological disorders, respiratory diseases, neurological disorders and urological disorders in a mammal, e.g. humans (preferably), dogs, cats, cows, horses, rabbits, and monkeys. This sequence represents human GPR35.

XX SQ Sequence 309 AA;

Query Match 100.0%; Score 1614; DB 9; Length 309;

Best Local Similarity 100.0%; Pred. No. 3.1e-167;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNGTYNTCGSSDLTWPAPKLGFAVYLVGLVLLNSLALVWFCRQMQWTETRIYMT 60
 DB 1 MNGTYNTCGSSDLTWPAPKLGFAVYLVGLVLLNSLALVWFCRQMQWTETRIYMT 60
 OY 61 NLAVALDCLLCTLPFVLSLRDTSPTPLCQLSQGLYLTNRYSISLVTAIVDRYAVRH 120

Db 61 NLAVALDCLLCTLPFVLSLRDTSPTPLCQLSQGLYLTNRYSISLVTAIVDRYAVRH 120

OY 121 PLRARGLSRPRQAAVCAVWLVLVIGSLVARWLLGIQEGGFCFRTRNFNMRPPLLG 180

Db 121 PLRARGLSRPRQAAVCAVWLVLVIGSLVARWLLGIQEGGFCFRTRNFNMRPPLLG 180

OY 181 YLPLAVVVFCSLKVTALAQRPPTDVGQAETRAKAAWMAWLVVVCFLPLHVLTVR 240

Db 181 YLPLAVVVFCSLKVTALAQRPPTDVGQAETRAKAAWMAWLVVVCFLPLHVLTVR 240

OY 241 LAVGNWACALLETIRRALVITSLKSDANCCLDIAICVYMAKFEQASALAVAPRAKHS 300

Db 241 LAVGNWACALLETIRRALVITSLKSDANCCLDIAICVYMAKFEQASALAVAPRAKHS 300

OY 301 QDSLVCVTLA 309

Db 301 QDSLVCVTLA 309

RESULT 9

ABG95172

ID ABG95172 standard; protein; 309 AA.

XX AC ABG95172;

XX DT 04-DEC-2002 (first entry)

XX DE Human GPCR GPR35 mutant A216K.

XX KW Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy; hypertension; reflux disease; depression; migraine; schizophrenia; ulcer; psychotonic disorder; asthma; bronchospasm; anaesthesia; myocardial infarction; MI; stroke; glaucoma; anxiety; prostatic hypertrophy; epilepsy; prostate cancer; rhinitis; angina; prostatic hypertrophy; receptor; mutant; mutin.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN W0200268600-A2.

XX PD 06-SEP-2002.

XX PF 26-FEB-2002; 2002MO-US005625.

XX PR 26-FEB-2001; 2001US-0271913P.

XX PA (AREN-) ARENA PHARM INC.

XX PI Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN; Lin I, Ortuno D;

XX DR WPI; 2002-706980/76.

XX DR N-PSDB; ABS73401.

XX PT New human G-protein coupled receptor (GPCR), useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR.

XX PS Example 2; Page 189-190; 201pp; English.

XX CC The present invention relates to transmembrane receptors, particularly endogenous human G-protein coupled receptors (GPCRs), mutant (non-endogenous) versions of the GPCRs, and the polynucleotide sequences encoding them. The GPCRs are useful for screening agonist or inverse agonist compounds for treating diseases associated with GPCR. Diseases that can be treated with such compounds include allergies, hypertension, reflux disease, depression, migraine, schizophrenia, ulcers, psychotonic disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI), stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer, anxiety, prostatic hypertrophy, rhinitis, and angina. The present sequence represents a mutant human GPCR

III

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RESULT 11
ADF70461
ID ADF70461 standard; protein; 547 AA.
XX
AC ADF70461;
XX
DT 12-FEB-2004 (first entry)
XX
DE Orphan receptor ligand-related human protein SeqID84.
XX
KW ligand; orphan receptor protein; fusion protein; fluorescent protein;
KW cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
KW GFPuv; Enhanced GFP; EGFP; human.
XX
OS Homo sapiens.
XX
PN WO2003071272-A1.
XX
PD 28-AUG-2003.
XX
PF 21-FEB-2003; 2003WO-JP001901.
XX
PR 22-FEB-2002; 2002JP-00045728.
PR 23-JUL-2002; 2002JP-00213949.
PR 11-OCT-2002; 2002JP-00298237.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;
XX
WPI; 2003-697654/66.
XX
DR N-PSDB; ADF70563.
XX
XX
PT Transformation of cells with a fusion protein of an orphan receptor
PT ligand with a fluorescent protein useful for identification of ligands
PT to the orphan receptor.
XX
PS Disclosure; SEQ ID NO 84; 594pp; Japanese.
XX
CC This invention relates to a novel method of identifying ligands to an
CC orphan receptor protein which comprises transforming cells with DNA
CC encoding a fusion protein of the orphan receptor with a fluorescent
CC protein, so that the fusion protein is expressed in the cells (or cell
CC membranes isolated from them) and contacting the cells with the potential
CC ligand to be tested. A suitable fluorescent protein for incorporation in
CC the fusion protein is green fluorescent protein (GFP), for example GFP-1,
CC wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the
CC identification of ligands binding to an orphan receptor protein.
XX
SQ Sequence 547 AA;
Query Match 99.6%; Score 1608; DB 7; Length 547;
Best Local Similarity 99.7%; Pred. No. 2.8e-166;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNGTYNTCGSSDLTWPFAIKLGFYAYLGVLVLGLLNSLALWVFCRMOQWTEIRYMT 60
DB 1 MNGTYNTCGSSDLTWPFAIKLGFYAYLGVLVLGLLNSLALWVFCRMOQWTEIRYMT 60
QY 61 NLAVADLCLLCTLPFFVHLSLSDTPTPLQSLQGIYLTNRYSISLVTAIAVDYVAVRH 120
DB 61 NLAVADLCLLCTLPFFVHLSLSDTPTPLQSLQGIYLTNRYSISLVTAIAVDYVAVRH 120
QY 121 PLRARGLRPRQAAAVCAVLWLVISLVARMLLGIQGGFCFRSTRHNFNSMRPPLLGF 180
DB 121 PLRARGLRPRQAAAVCAVLWLVISLVARMLLGIQGGFCFRSTRHNFNSMRPPLLGF 180
QY 181 YLPLAVVVFCSLKVVTALQRPPTDVGQAEATKAAKMWANLLVFWCFLPLHVLITVR 240
DB 181 YLPLAVVVFCSLKVVTALQRPPTDVGQAEATKAAKMWANLLVFWCFLPLHVLITVR 240
QY 241 LAVGNACALLETIRRALYITSKLSANCLDAICYVYMAKEFQASALAVAPRAKAHKS 300
DB 241 LAVGNACALLETIRRALYITSKLSANCLDAICYVYMAKEFQASALAVAPRAKAHKS 300
QY 301 QDSLVCVTLA 309
DB 301 QDSLVCVTLA 309
RESULT 12
ADF50511
ID ADF50511 standard; protein; 309 AA.
XX
AC ADF50511;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human GPCR GPR35 D113A mutein (SeqID 191).
XX
KW mutant; mutein; transformation; endocrine cell line;
KW expression cloning system; bioactive peptide; GPCR ligand; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 113 /note= "Wild type Asp substituted by Ala"
FT
XX
PN WO2003087366-A1.
XX
PD 23-OCT-2003.
XX
PF 16-APR-2003; 2003WO-JP004840.
XX
PR 16-APR-2002; 2002JP-00113030.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Sasaki K, Miura K, Saeki S, Yoshizawa M, Kishimoto K, Kunitomo H;
PI Nishi T, Obinata M;
XX
WPI; 2003-833737/77.
XX
XX
Endocrine cell lines originated from mammalian hypothalamus and
pancreatic islet, applicable in expression cloning systems of bioactive
peptide precursor genes, and in screening G protein-coupled receptor
ligands.
XX
XX
Example 24; SEQ ID NO 191; 316pp; Japanese.
XX
XX
This invention relates to a novel method for obtaining a DNA that encodes
a peptide acting as agonist, antagonist or inverse agonist on a target
receptor. Specifically, it comprises transformation of endocrine cell
lines originating from mammalian hypothalamus and pancreatic islets,
culturing the transformants and contacting with cells expressing the
target receptor. The identification of those cells with a response
reaction can be used for selecting a transformant cell line with the
appropriate target activity that is expressing the novel transformed DNA.
Accordingly, the present invention describes novel cell lines that are
applicable in expression cloning systems of bioactive peptide precursor
genes, and in screening GPCR ligands for use as drugs including agonists,
antagonists and inverse agonists i.e. activators and inhibitors. Such
cell lines can provide a highly sensitive and convenient GPCR ligand
assay system. This polypeptide sequence is the human GPCR GPR35 D113A
mutein of the invention.
XX
SQ Sequence 309 AA;
Query Match 99.5%; Score 1606; DB 7; Length 309;
Best Local Similarity 99.7%; Pred. No. 2.3e-166;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNGTYNTCGSSDLTWPFAIKLGFYAYLGVLVLGLLNSLALWVFCRMOQWTEIRYMT 60
DB 1 MNGTYNTCGSSDLTWPFAIKLGFYAYLGVLVLGLLNSLALWVFCRMOQWTEIRYMT 60
```

Db 1 MNGTYNTCGSSDLTWPPAIAKLGFAVYGLVLLVGLLLNSLALWVFCRCMQWTETRIYMT 60
QY 61 NLAVADLCCLCTLPVLSHSDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDVAVRH 120
Db 61 NLAVADLCCLCTLPVLSHSDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDVAVRH 120
QY 121 PLRAGLRSPQAAAVCAVAVLWLVIGSLVARWLLGIQEGGFCFRSTRNFNSMRPPLIGF 180
Db 121 PLRAGLRSPQAAAVCAVAVLWLVIGSLVARWLLGIQEGGFCFRSTRNFNSMRPPLIGF 180
QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGOAEATRKAAARMVWVNLVVFVCFPLPHVGLTVR 240
Db 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGOAEATRKAAARMVWVNLVVFVCFPLPHVGLTVR 240
QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDIAICYTMAKEFQASALAVAPRAKAKHS 300
Db 241 LAVGNACALLETIRRALYITSKLSDANCCLDIAICYTMAKEFQASALAVAPRAKAKHS 300
QY 301 QDSLVCVTILA 309
Db 301 QDSLVCVTILA 309

RESULT 13

AAY58645

ID AAY58645 standard; protein; 309 AA.

XX AAY58645;

AC AAY58645;

XX AAY58645;

DT 11-APR-2000 (first entry)

XX 11-APR-2000 (first entry)

DE Human G-protein coupled receptor GPR35A.

XX GPR35A; human; G-protein coupled receptor; purinergic;

KW 7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic;
KW cytotatic; antidiabetic; anorectic; antiasthmatic; antiparkinsonian;
KW hypertensive; hypertensive; osteopathic; antitanginal; cardiac;
KW cerebroprotective; antiulcer; antiallergic; antimigraine; antiemetic;
KW tranquilizer; antidepressant; neuroleptic; nootropic; anticonvulsant;
KW therapy; diagnosis; vaccine.

XX Homo sapiens.

OS Homo sapiens.

XX WO964452-A1.

PN WO964452-A1.

XX 16-DEC-1999.

PD 16-DEC-1999.

XX 01-JUN-1999; 99WO-US012123.

PF 01-JUN-1999; 99WO-US012123.

XX 11-JUN-1998; 98US-00096031.

PR 11-JUN-1998; 98US-00096031.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX Elshourbagy NA;

PI Elshourbagy NA;

XX WPI; 2000-116525/10.

DR N-PSDB; AA235390.

XX New human GPR35A polypeptides and polynucleotides used to identify

PT agonists, antagonists and inhibitors for use in therapy.

PT agonists, antagonists and inhibitors for use in therapy.

XX Claim 1; Page 32-33; 38pp; English.

PS Claim 1; Page 32-33; 38pp; English.

XX The present sequence represents human GPR35A, a novel member of the

CC purinergic family of polypeptides and a G-protein coupled receptor. The

CC invention provides GPR35A polypeptides having at least 70% identity with

CC the present sequence, GPR35A polynucleotides, recombinant materials, and

CC methods for their production. GPR35A polypeptides can be used for

CC identifying agonists and antagonists/inhibitors, and for detecting

CC diseases associated with inappropriate GPR35A activity or levels. GPR35A

CC polypeptides and polynucleotides, agonists, antagonists and antibodies

CC are used to treat: infections such as bacterial, fungal, protozoan and

CC viral infections, particularly HIV-1 and HIV-2; pain; cancer; diabetes;

CC obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart
CC failure; hypotension; hypertension; urinary retention; osteoporosis;
CC angina pectoris; myocardial infarction; stroke; ulcers; allergy; benign
CC prostatic hypertrophy; migraine; vomiting; psychotic and neurological
CC disorders including anxiety, schizophrenia, manic depression, depression,
CC delirium, dementia and severe mental retardation; and dyskinesias such as
CC Huntington's or Gilles de la Tourette's syndrome. The polypeptide is also
CC useful for production of vaccines

XX Sequence 309 AA;

SQ Sequence 309 AA;

Query Match 99.3%; Score 1602; DB 3; Length 309;

Best Local Similarity 99.4%; Pred. No. 6.3e-166;

Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIAKLGFAVYGLVLLVGLLLNSLALWVFCRCMQWTETRIYMT 60

Db 1 MNGTYNTCGSSDLTWPPAIAKLGFAVYGLVLLVGLLLNSLALWVFCRCMQWTETRIYMT 60

QY 61 NLAVADLCCLCTLPVLSHSDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDVAVRH 120

Db 61 NLAVADLCCLCTLPVLSHSDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDVAVRH 120

QY 121 PLRAGLRSPQAAAVCAVAVLWLVIGSLVARWLLGIQEGGFCFRSTRNFNSMRPPLIGF 180

Db 121 PLRAGLRSPQAAAVCAVAVLWLVIGSLVARWLLGIQEGGFCFRSTRNFNSMRPPLIGF 180

QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGOAEATRKAAARMVWVNLVVFVCFPLPHVGLTVR 240

Db 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGOAEATRKAAARMVWVNLVVFVCFPLPHVGLTVR 240

QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDIAICYTMAKEFQASALAVAPRAKAKHS 300

Db 241 LAVGNACALLETIRRALYITSKLSDANCCLDIAICYTMAKEFQASALAVAPRAKAKHS 300

QY 301 QDSLVCVTILA 309

Db 301 QDSLVCVTILA 309

RESULT 14

ADA84069

ID ADA84069 standard; protein; 309 AA.

XX ADA84069;

AC ADA84069;

XX 20-NOV-2003 (first entry)

DT 20-NOV-2003 (first entry)

DE Human GPR35 protein.

XX human; marker; expressed sequence tag; EST; arabinidopsis; tumour;

KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;

KW vaccine.

XX Homo sapiens.

OS Homo sapiens.

XX WO2002103028-A2.

PN WO2002103028-A2.

XX 27-DEC-2002.

PD 27-DEC-2002.

XX 30-MAY-2002; 2002WO-IB004189.

PF 30-MAY-2002; 2002WO-IB004189.

XX 30-MAY-2001; 2001US-0293999P.

PR 22-OCT-2001; 2001US-0330457P.

PR 19-FEB-2002; 2002US-0357144P.

XX (BIOM-) BIOMEDICAL CENT.

PA (BIOM-) BIOMEDICAL CENT.

PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;

XX WPI; 2003-175241/17.

DR N-PSDB; ADA84068.

XX

PT Determining if a nucleic acid is a marker for a phenotype/cell type of
PT interest, by global comparison of expressed sequence tags known to be
PT expressed in the phenotype/cell type with all ESTs expressed in normal
PT tissue.
XX
XX
XX Claim 29; Page 448-449; 516pp; English.
XX
XX The invention relates to a novel method for determining if a nucleic acid
CC is a marker for a predetermined phenotype/cell type of interest from a
CC biological species. The method comprises performing a global comparison
CC of a group of expressed sequence tags (ESTs) known to be expressed in the
CC phenotype/cell type of interest with all ESTs expressed in normal tissue
CC in order to identify ESTs that are preferentially expressed in the
CC phenotype/cell of interest. A method of the invention is useful for
CC determining whether a nucleic acid is a marker for a predetermined
CC phenotype or cell type of interest from a biological species, preferably
CC Arabidopsis or human. The cell type of interest is an abnormal cell such
CC as a tumour cell, and the predetermined phenotype is a stress-induced
CC phenotype such as hyperosmotic stress or high salt conditions. A method
CC of the invention is also useful for determining the progression of colon
CC cancer in a human, for detecting a tumour cell, and for regulating or
CC preventing the growth of a tumour cell. An antibody of the invention is
CC useful for detecting the absence or presence of peptides encoded by
CC tumour-associated markers. A polypeptide of the invention is useful as an
CC immunogen for vaccinating an animal. The present sequence represents a
CC tumour-associated antigen of the invention.
XX
XX Sequence 309 AA;

Query Match 99.3%; Score 1602; DB 6; Length 309;
Best Local Similarity 99.4%; Pred. No. 6.3e-166;
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 60
DB 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 60
QY 61 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTIAVDYVAVRH 120
DB 61 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTIAVDYVAVRH 120
QY 121 PLRARGLSRPROAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLIGF 180
DB 121 PLRARGLSRPROAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLIGF 180
QY 181 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRAKARWVWVANLLVFVVCFLPLHVLTVR 240
DB 181 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRAKARWVWVANLLVFVVCFLPLHVLTVR 240
QY 241 LAVGNWACALLETTIRRALYITSKLSANCCCLDAICYTMAKBFQBSALAVAPRAKAHKS 300
DB 241 LAVGNWACALLETTIRRALYITSKLSANCCCLDAICYTMAKBFQBSALAVAPRAKAHKS 300
QY 301 QDSLCVTLA 309
DB 301 QDSLCVTLA 309

RESULT 15
ADO78095
ID ADO78095 standard; protein; 394 AA.
XX
XX ADO78095;
XX
XX 26-AUG-2004 (first entry)
XX
XX Human GPR35 isoform.
XX
XX tumour-associated antigen; TAG; cancer; lung cancer; breast cancer;
XX prostate cancer; colon cancer; stomach cancer; pancreatic cancer;
XX ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer;
XX melanoma; tumour; human; GPR35.
XX

OS Homo sapiens.
XX DE10254601-A1.
XX
XX 03-JUN-2004.
XX
XX 22-NOV-2002; 2002DE-01054601.
XX
XX 22-NOV-2002; 2002DE-01054601.
XX
XX (GANY-) GANYMED PHARM AG.
XX
XX Tuereci O, Sahin U, Koslowski M;
XX WPI; 2004-421820/40.
XX
XX Composition containing inhibitor of expression or activity of specific
PT tumor-associated antigens, useful for treating cancers, also related
PT compositions for diagnosis and monitoring.
XX
XX Claim 72; SEQ ID NO 10; 124pp; German.
XX
XX The invention relates to pharmaceutical compositions that comprise an
CC agent that inhibits the expression or activity of a tumour-associated
CC antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical
CC compositions and related compositions, are used for treatment of diseases
CC associated with (abnormal) expression of TAG, specifically cancer e.g. of
CC lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney
CC or cervix, also melanoma. Compositions containing TAG, or related nucleic
CC acid, antibodies or host cells, are also useful for diagnosis and
CC monitoring of tumours. The present sequence represents the amino acid
CC sequence of a human GPR35.
XX
XX Sequence 394 AA;

Query Match 99.3%; Score 1602; DB 8; Length 394;
Best Local Similarity 99.4%; Pred. No. 8.5e-166;
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 60
DB 86 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 145
QY 61 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTIAVDYVAVRH 120
DB 146 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTIAVDYVAVRH 205
QY 121 PLRARGLSRPROAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLIGF 180
DB 206 PLRARGLSRPROAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLIGF 265
QY 181 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRAKARWVWVANLLVFVVCFLPLHVLTVR 240
DB 266 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRAKARWVWVANLLVFVVCFLPLHVLTVR 325
QY 241 LAVGNWACALLETTIRRALYITSKLSANCCCLDAICYTMAKBFQBSALAVAPRAKAHKS 300
DB 326 LAVGNWACALLETTIRRALYITSKLSANCCCLDAICYTMAKBFQBSALAVAPRAKAHKS 385
QY 301 QDSLCVTLA 309
DB 386 QDSLCVTLA 394

Search completed: February 9, 2006, 00:54:42
Job time : 220.5 secs

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OM protein - protein search, using sw model

Run on: February 9, 2006, 00:55:13 ; Search time 26.5 Seconds
(without alignments)
1121.924 Million cell updates/sec

Title: US-10-083-168-16
Perfect score: 1614
Sequence: 1 MNGYNTCGSSDLTPPAIK.....AVAPRAKHSQDSLCVTLA 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	401	24.8	370	JC5549	heptahelical P2Y5-
2	368.5	22.8	308	I50241	G protein-coupled
3	368.5	22.8	387	I69202	G protein-coupled
4	360.5	22.3	344	T09508	intron 17 purinerg
5	319	19.8	328	I55450	G protein-coupled
6	319	19.8	373	A47556	ATP receptor P2u -
7	318	19.7	362	S33733	G protein-coupled
8	315.5	19.5	365	S68679	G protein-coupled
9	312.5	19.4	364	JQ1488	bradykinin B2 rece
10	312.5	19.4	366	1 OORTB2	bradykinin recepto
11	310	19.2	342	S13638	platelet-activatin
12	308.5	19.1	375	A54946	P-2U nucleotide re
13	305.5	18.9	354	I53033	G protein-coupled
14	305.5	18.9	362	A57641	G protein-coupled
15	305	18.9	352	S60024	bradykinin B1 rece
16	304	18.8	342	A40191	platelet-activatin
17	302.5	18.7	362	B57641	G protein-coupled
18	302.5	18.7	373	JC4162	P2Y receptor - bov
19	301.5	18.7	362	S68207	G protein-coupled
20	298.5	18.5	373	JC4737	G protein-coupled
21	293	18.2	341	JC43252	platelet-activatin
22	291	18.0	328	JC4800	P2Y6 receptor - hu
23	289	17.9	363	JC2543	angiotensin II rec
24	288.5	17.9	352	A43113	chemokine (C-C) re
25	285.5	17.7	361	B45680	platelet activatin
26	283	17.5	341	S63666	bradykinin B2 rece
27	281.5	17.4	366	I49519	somatostatin recep
28	279.5	17.3	363	I57955	somatostatin recep
29	279.5	17.3	364	JN0763	somatostatin recep

ALIGNMENTS

RESULT 1

JC5549
heptahelical P2Y5-like receptor - human
C/Species: Homo sapiens (man)
C/Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C/Accession: JC5549
R/Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.
Biochem. Biophys. Res. Commun. 236, 106-112, 1997
A/Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.
A/Reference number: JC5549; MUID:97366605; PMID:9223435
A/Accession: JC5549
A/Molecule type: DNA
A/Residues: 1-370 <JAN>
A/Cross-references: UNIPROT:Q99677; UNIPARC:UPI000016A4CA; DDBJ:AF005419; NID:G2240034;
C/Superfamily: ATP receptor P2u

Query Match 24.8%; Score 401; DB 2; Length 370;
Best Local Similarity 34.0%; Pred. No. 1.9e-29;
Matches 105; Conservative 58; Mismatches 104; Indels 42; Gaps 11;

QY	25	AYLGVLVLLNSLALWVFCRQQWTERIYVNTNLAVALDLCLTLPP-VLHSLR--	81
DB	44	AVYSVVFILGILTNSVLSLVFVCFRMRSETAIFITNLAVSDLLFVCTLPFKIFYNRHH	103
QY	82	-DTSYPLCOLSQGIYLTNRYMSISLVTAIAVDVVAVRHPLRGLRSPROAAVCAVL	140
DB	104	WPFQDT-LCKISGTAFLTNIGSMLFLTCISVDRLAIVYPPRSRTIRTRNSAIVCAGV	162
QY	141	WVLVIGSLVARWLLGIQGGF-----CFR-----STRHFNFSMRFPPLGPLYL	182
DB	163	WILVLSG-----GISLSFTNNVNNATTCFGLSKRVKTYLSKITIFIEVVGFII	215
QY	183	PLAVVVFCSLKVVTALQRPPTDVGQABAT-RKAARMVWNLVLFVFCPLPHVGLTVRL	241
DB	216	PLILNVSCSSVVLRTL--RKPATLSQIGTNKKKVLKMTVHMAVFCVFPVNSVLFYA	273
QY	242	AVGWAC--ALLETTRALY-ITSKLSDNACCLDAICYVMKAKEQESALAVAPRAKAH	298
DB	274	LVRSQAITNCFERFAKIMYPITCLATLNCDFPFIFYFTLESFQKSFYI-----NAH	327
QY	299	KSQDSILCVT 307	
DB	328	RMESLFT 336	

RESULT 2

I50241
G protein-coupled receptor 6H1 - chicken
N/Alternate names: purinoceptor 6H1
C/Species: Gallus gallus (chicken)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: I50241; JC4618

R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A;Title: Identification of a G protein coupled receptor induced in activated T cells.
A;Reference number: I50241; MUID:93329058; PMID:8393036
A;Accession: I50241
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-308 <XAP>
A;Cross-references: UNIPROT:P32250; UNIPARC:UPI0000055A6B; GB:L06109; NID:G304383; PIDN:
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Reference number: JC4618; MUID:96190677; PMID:8619790
A;Accession: JC4618
A;Molecule type: mRNA
A;Residues: 1-308 <WEB>
A;Cross-references: UNIPARC:UPI0000055A6B; GB:L06109; NID:G304383; PIDN:AAB06587.1; PID:
A;Experimental source: T-cells
A;Comment: This receptor plays a role in T-cell activation.
C;Genetics:
A;Gene: p2y5
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
F;15-40/Domain: transmembrane #status predicted <TM1>
F;51-74/Domain: transmembrane #status predicted <TM2>
F;89-109/Domain: transmembrane #status predicted <TM3>
F;133-153/Domain: transmembrane #status predicted <TM4>
F;177-201/Domain: transmembrane #status predicted <TM5>
F;227-248/Domain: transmembrane #status predicted <TM6>
F;269-292/Domain: transmembrane #status predicted <TM7>

Query Match 22.8%; Score 368.5; DB 2; Length 308;
Best Local Similarity 30.3%; Pred. No. 1.6e-26;
Matches 91; Conservative 64; Mismatches 102; Indels 43; Gaps 10;

QY 10 SSDLTWPPAIKLGFY-AYLGVLAVLGLLSLALWVFCRCMQQWETRIYMTNLAVADLC 68
Db 3 SSSCTEDSKFYLYGCVFSWVFLGLIACVAYIIFTLKVRNNTTYMLMLAISDLL 62

QY 69 LLCTLPFVLHSLRDTSTP-----LCQLSQGIYLTNRYSISLVTAIAVDYVAVRHPLRA 124
Db 63 FVFTLPFRIFYF-VVRNWPFGDLCKISVTLFTYNNYGSILPLTCSVDRFLAIVHPFS 121

QY 125 RGLRSPROAAVCAVLWLVVI-GSLVARMLLGIQGGFCFRST-RNFNSMR-----FP- 176
Db 122 KTLRTKRNARIVCAVWITVLASTPSF-----FQSTNRQNTEQRTCFENFPE 171

QY 177 -----LLGFVPLAVVFCSLKVVTALAQRPPTDVQAEATKAAARMWA 221
Db 172 STWKTYLSRIVPIEIVGFPIPLINVTCTMVLRTL-NKPLTSLRNKLSKKVLMKIFV 230

QY 222 NLIVFVVCFLPHVGL---TVRLAVGNACALLTERRALYITSKLSDANCCLDAICYX 278
Db 231 HLIVFCFCFVPYNTILILSLMETQWINGSVVTARTWYPVTLCAVSNCCFDPVIVYF 290

RESULT 3
I69202
G protein-coupled receptor HM74 - human
C;Species: Homo sapiens (man)
A;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I69202
R;Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chem
A;Reference number: I54751; MUID:94026229; PMID:7505609
A;Accession: I69202
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-387 <RES>
A;Cross-references: UNIPROT:P49019; UNIPARC:UPI0000043C3C; GB:D10923; NID:G219866; PIDN:
C;Genetics:
A;Gene: HM74

C;Superfamily: G protein-coupled receptor 4

Query Match 22.8%; Score 368.5; DB 2; Length 387;
Best Local Similarity 34.3%; Pred. No. 2.1e-26;
Matches 95; Conservative 48; Mismatches 105; Indels 29; Gaps 11;

QY 27 LGVLAVLGLLSLALWVFCRCMQQWETRIYMTNLAVADLCCLTLPVL-----HSRLR 81
Db 34 LGLEPIFGLLGLNGLALWIFCHLKSWSKSRIFLFLNLAADFLIIICLPFVMDYVYRRSDW 93

QY 82 DTSDFPLCQLSQGIYLTNRYSISLVTAIAVDYVAVRHPLRARGLRSPROAAVCAVLW 141
Db 94 NFGDIP-CELVLFEMAMNRQSGIIFLTVAVDVRVVRVPHALNKISNWTAAITISCLLM 152

QY 142 VLVIQ---SLVARMLLGIQGG-GFCFR-STRHNF--NSMRFPPLGFLPLAVVFCSLK 193
Db 153 GITVGLTVHLLKKLL-LQNGPANVCISFSICHTFRWEAMF-LLEFLPLGLIILFCSAR 210

QY 194 VVTALAQRPPTDVQAEATKAAARMVWNLVFCFLPLHVLGTLVRLAVGW-----N 246
Db 211 IISLSRQ---QMDRHAKIKRAITFIMVAVIVFICPLP---SVVVRIRIFMLHTSGTQ 264

QY 247 ACALLETIRRALYITSKLSDANCCLDAICYXMAKEF 283
Db 265 NCEVRSVDLAPFILTSTYNNMLDPVVYFSSPSP 301

RESULT 4
T09508
Intron 17 purinergic receptor P2Y5 - human
N;Alternate names: G-protein coupled receptor
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09508
R;Bohm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.
submitted to the EMBL Data Library, April 1997
A;Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinob
A;Reference number: Z16705
A;Accession: T09508
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-344 <BOH>
A;Cross-references: UNIPROT:P43657; UNIPARC:UPI000005041B; EMBL:AF000546; NID:G2232068; I
C;Genetics:
A;Map position: 13
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 22.3%; Score 360.5; DB 2; Length 344;
Best Local Similarity 29.2%; Pred. No. 1e-25;
Matches 90; Conservative 68; Mismatches 107; Indels 43; Gaps 10;

QY 10 SSDLTWPPAIKLGFYAYL-GVLLVLGLLSLALWVFCRCMQQWETRIYMTNLAVADLC 68
Db 6 SSHCFYNSFKTYLGCMSWVFLGLVSNCAIYIFICLVKVRNNTTYMLNLAISDLL 65

QY 69 LLCTLPFVLHSLRDTSTP-----LCQLSQGIYLTNRYSISLVTAIAVDYVAVRHPLRA 124
Db 66 FVFTLPFRIFYF-TTRNWPFGDLCKISVMLPYTNMYGSILPLTCSVDRFLAIVVPPKS 124

QY 125 RGLRSPROAAVCAVLWLVVI-GSLVARMLLGIQGG-----FCFRSTRHNFNSMRFP-- 176
Db 125 KTLRTKRNARIVCTGVMLTVIGGSAPAVFVOSTHSGNNAEACFEN-----FPBA 175

QY 177 -----LLGFVPLAVVFCSLKVVTALAQRPPTDVQAEATR-KAARMWA 221
Db 176 TWKTYLSRIVPIEIVGFPIPLINVTCTSSWVLTLLTK--PVTLSRKINKTKVLMKIFV 233

QY 222 NLIVFVVCFLPHVGLTVRLAVGNWNA---CALLETIRRALYITSKLSDANCCLDAICYX 278
Db 234 HLIVFCFCFVPYNTILILYSLVTRTQTFVNCVSWAAVTRMYPITLCAVSNCCFDPVIVYF 293

QY 279 MAKEFQEA 286

QY	45	FCRCMQQWTEFRIYMTNLAVADLCILCTPLPVLHSLRDTSD---TFLCQLSQGIYLTNR	10
DB	65	FVFHMRPMSGISVYMFNLALADFLVLTLPALIFYYFNKTDWIFGDMCKLQRFIFHWL	124
QY	101	YMSISLVTATAIVDRYVAVRHPLRARGLSRQAAAVCAVLWLVLTGSLVARMLL---	GI 156
DB	125	YGSILPLFCISVHRVTGVVHPLKSLGRUKKNNAVYSSLVMAVLV-AVIAPILFYSGTGV	183
QY	157	QEGG--FCFRSTRHNF-----NSMRPFLGLGYLPLAVVVPFCSLKVTALAQRPPTDVQ	208
DB	184	RNNKTIITCVDTADEYLSRSFYFYSMCTTVFMFCIPFVILGCGYGLVAKLIYK---	DLDN 240
QY	209	AEATKKAARMYWANLLVFVCFPLPHVGLITVPLAVGWN-----ACALLTETIRREALYITS	263
DB	241	SPLRRKSIYLIIVLITVFAVSYPFHVMKLTNLRDLDFQTQMCAFNDEKVVATYQVTRG	300
QY	264	LSDMANCLDAICYYNMAKEFOEASALAVAPRAKAHKSQDSL	304
DB	301	LASLNSCVDPILYFLAGTFFR--RLSRATKRSSRRSEPNV	339

RESULT 8

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-342 <HON>
A:Cross-references: UNIPROT:P21556; UNIPARC:UPI00001311ER; GB:X56736; NID:q49442; PIDN:
A:Note: the species of guinea pig is not identified; in Genbank entry CCPAFREC, release
C:Superfamily: ATP receptor P2u

Query Match 19.2%; Score 310; DB 2; Length 342;
Best Local Similarity 28.2%; Pred. No. 4.7e-21;
Matches 81; Conservative 58; Mismatches 110; Indels 38; Gaps 9;

Qy 29 VLVGLGLNLSLWVFCRMM--QOWTETRIYMTNLAVALDCLLCTLP--FVLHSLRDT 83
Db 24 IIFVLGIANGVWVWF-ARLYPSKLNLEIKIFMWNLTVDADLLFLITPLWIVYYSQGN 82
Qy 84 SDTP--LQLSQGIYLTNRYSISLVTAADVRYAVRHLRARGLSRQQAACVAVLW 141
Db 83 WFLPKFLCNLAGCLFFINTYCSVAFGLVITYNRFOAVKYPITKAQATRKRGIALSLVIW 142
Qy 142 VLVGSLVARWLLGQEQ-----GGFCFSTRNFNSMRPPL-----LGFYPLA 185
Db 143 VAIWAA--ASFLVMDSTNVSNKAGSGNITRCFEHYEKGSKPVLIIHICIVLGGFFIVFL 200
Qy 186 VVFCGLKVTALAQRPPTDVQGAETRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGW 245
Db 201 LILFCNLVIIHTLRQPKVQORNAEVRERLMMVCTVLAVFVICFVPHM-----VOLPW 255
Qy 246 NACAL-----LETIRRAYITSKLSDANCCLDALCIYYMAKEFQE 285
Db 256 TLAEGLMWPSSNHQAINDAHQVTLCLLSTNCVLDPIVYCFLTKKFKK 302

RESULT 12
A54946
P-2U nucleotide receptor - human
C:Species: Homo sapiens (man)
C>Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1999
C:Accession: A54946
R:Parrr, C.B.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J.C
Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994
A>Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cystic
A:Reference number: A54946; MUID:94211846; PMID:8159738
A:Accession: A54946
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-375 <PAR>
A:Cross-references: UNIPARC:UPI0000145104; GB:U07225
A:Note: parts of this sequence were confirmed by protein sequencing
C:Genetics:
A:Gene: GDB:P2RY2; HP2U; P2U
A:Cross-references: GDB:362713; OMIM:600041
A:Map position: 11q13.5-11q14.1
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.1%; Score 308.5; DB 2; Length 375;
Best Local Similarity 31.7%; Pred. No. 7.1e-21;
Matches 89; Conservative 41; Mismatches 104; Indels 47; Gaps 8;

Qy 28 GVLVGLGLNLSLWVFCRMMQOWTETRIYMTNLAVALDCLLCTLPFVLHSLRDTSDTP 87
Db 41 GVVCVGLCLNAGVLYFICRLKTWASTTYMNFHLAVSDALYAASLPLVLYYARGDHP 100
Qy 88 ----LQLSQGIYLTNRYSISLVTAADVRYAVRHLRARGLSRQQAACVAVLW 143
Db 101 FSTVLCIKVRFLEYTNLYSILFLTCISVHRCGLVPLRSLRNGRARYARRVAGAVWL 160
Qy 144 VTGSLVARWLLGQEGGFCFRSTRNFNSMRPPL-----LGF 180
Db 161 V-----LACQAPVLYFVTT-----SARGPLTCHDTSAPELFSREYVSSVMGLLF 206
Qy 181 YLPLAVVWFCSLKVTALAQRPPT--TDVQGAETRKAARMVWANLLVFVVCFLPLHVGLT 238
Db 181 YLPLAVVWFCSLKVTALAQRPPT--TDVQGAETRKAARMVWANLLVFVVCFLPLHVGLT 238

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Db 207 AVPFVAVLVVYVLMARLL-LKPAYTSGGLPRAKRKSVRTIAVVLAVFALCFLPFHVTRT 265
QY 239 VRLAVGW--NACALLTIRRALYITSKLSDANCLDAICY 277
Db 266 LYTSPRSLDLSCHTLNAINNA-YKVRLASANCLDPVLYF 305

RESULT 13
I53033
G protein-coupled receptor - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
R;Heiber, M.; Docherty, J.M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng, H.H.Q.; Marchese, A
DNA Cell Biol. 14, 25-35, 1995
A;Title: Isolation of three novel human genes encoding G protein-coupled receptors.
A;Reference number: I53033; MUID:95134353; PMID:7832990
A;Accession: I53033
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-354 <RES>
A;Cross-references: UNIPROT:P46093; UNIPARC:UPI0000016A9DF; GB:L36148; NID:g598152; PIDN:
C;Superfamily: G protein-coupled receptor 4
C;Keywords: G protein-coupled receptor

Query Match 18.9%; Score 305.5; DB 2; Length 354;
Best Local Similarity 31.0%; Pred. No. 1.3e-20;
Matches 93; Conservative 48; Mismatches 118; Indels 41; Gaps 11;

QY 2 NGTYNTC---GSSDLTWPPAIKLGFAVYLVGLVLLNSLALWVFCRCMQQTETRIY 58
Db 3 NHTWEGCHVDSRVDLHLPFPPSL-----YIFVIGV-GLPTNCLALWAAYRQVQRNELGVY 55

QY 59 MTNLAVADLCLLCTLP-----FVLHSLRDTSDTLPCLQSQGIYLTNRYSISLVTAIAVDR 114
Db 56 LMNLSTADLLYICTLPLWVDYFLHNDNWIHGPSCKLFGFIFTNIIYISIAFLCCISVDR 115

QY 115 YVAVRHPLRARGLRSPQAAACAVLVLVLSVARWLLGLOEGGFCFRST-RHNFNSM 173
Db 116 YLAVAHPLRPARLRVKTAVAVSSVWATLANSAP--LFHDE---LFRDRYNTHTFCPE 170

QY 174 RPPL-----LGFYLPVAVVFCSLKVVTALAQRPPTDVGOAEATRKAAARMW 220
Db 171 KFPMEGWAMNLYRVFVGLFPWMLLSYRGILRAVGSVST---ERQEKAKIKRLAL 227

QY 221 ANLLVFFVCFPLHVLGLTVRLAV-----GNACALLETIRRALYITSKLSDANCLDAICY 276
Db 228 SLTIAVLVCFAPYHVLLLSRSALYLGPRWD-CGFEERVFSAYHSSLAFTSLNCVADPILY 286

RESULT 14
A57641
G protein-coupled receptor 4 - human
C;Species: Homo sapiens (man)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
R;Mahadevan, M.S.; Baird, S.; Bailly, J.E.; Shutler, G.G.; Sabourin, L.A.; Tailfidi, C.
Genomics 30, 84-88, 1995
A;Title: Isolation of a novel G protein-coupled receptor (GPR4) localized to chromosome
A;Reference number: A57641; MUID:96129306; PMID:8595909
A;Accession: A57641
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-362 <NAH>
A;Cross-references: UNIPROT:P46093; UNIPARC:UPI0000050428; GB:U21051; NID:g687793; PIDN:
C;Genetics:
A;Gene: GPR4
A;Cross-references: GDB:371710; OMIM:600551
A;Map position: 19q13.3-19q13.3
A;Introns: #status absent
C;Superfamily: G protein-coupled receptor 4
C;Keywords: G protein-coupled receptor
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Query Match 18.9%; Score 305.5; DB 2; Length 362;
Best Local Similarity 31.0%; Pred. No. 1.3e-20;
Matches 93; Conservative 48; Mismatches 118; Indels 41; Gaps 11;

QY 2 NGTYNTC---GSSDLTWPPAIKLGFAVYLVGLVLLNSLALWVFCRCMQQTETRIY 58
Db 3 NHTWEGCHVDSRVDLHLPFPPSL-----YIFVIGV-GLPTNCLALWAAYRQVQRNELGVY 55

QY 59 MTNLAVADLCLLCTLP-----FVLHSLRDTSDTLPCLQSQGIYLTNRYSISLVTAIAVDR 114
Db 56 LMNLSTADLLYICTLPLWVDYFLHNDNWIHGPSCKLFGFIFTNIIYISIAFLCCISVDR 115

QY 115 YVAVRHPLRARGLRSPQAAACAVLVLVLSVARWLLGLOEGGFCFRST-RHNFNSM 173
Db 116 YLAVAHPLRPARLRVKTAVAVSSVWATLANSAP--LFHDE---LFRDRYNTHTFCPE 170

QY 174 RPPL-----LGFYLPVAVVFCSLKVVTALAQRPPTDVGOAEATRKAAARMW 220
Db 171 KFPMEGWAMNLYRVFVGLFPWMLLSYRGILRAVGSVST---ERQEKAKIKRLAL 227

QY 221 ANLLVFFVCFPLHVLGLTVRLAV-----GNACALLETIRRALYITSKLSDANCLDAICY 276
Db 228 SLTIAVLVCFAPYHVLLLSRSALYLGPRWD-CGFEERVFSAYHSSLAFTSLNCVADPILY 286

RESULT 15
S60024
bradykinin B1 receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
A;Accession: S60024
R;MachNeil, T.; Bierilo, K.K.; Menke, J.G.; Hees, J.F.
Biochim. Biophys. Acta 1264, 223-228, 1995
A;Title: Cloning and pharmacological characterization of a rabbit bradykinin B(1) receptor
A;Reference number: S60024; MUID:96085127; PMID:7495867
A;Accession: S60024
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-352 <MAC>
A;Cross-references: UNIPROT:P48748; UNIPARC:UPI0000126ABF; EMBL:U20507; NID:g1041820; PII
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 18.9%; Score 305; DB 2; Length 352;
Best Local Similarity 26.6%; Pred. No. 1.4e-20;
Matches 89; Conservative 62; Mismatches 131; Indels 52; Gaps 10;

QY 7 TCGSSDLTWPPAIKLGFAVYLVGLVLLNSLALWVFCRCMQQTETRIYMTNLAVAD 66
Db 24 SCGAPDADWDLHRL-LPTFTIATITLGLLGNFVLSVFLARRRLSVAEIVLANLAASD 82

QY 67 LCLLCTLPFVLHSLRDTSDTP-----LCQLSQGIYLTNRYSISLVTAIAVDRVAVRHPL 122
Db 83 LVPVLGLPMAENVANQPDWPGALCRVNGVIKANLFISIFLVVAISQDRYSVLVHPM 142

QY 123 RARGLRSPQAAACAVLVLVLSVARWLLGLOEGGFCFRSTR-----167
Db 143 ASRRGRRRQAQCALIW--LAGGL-----LSTPTFVLSRAVPELNASACILLP 193

QY 168 -----HNFNSMRPPLGLGYLPVAVVFCSLKVVTAL---AQRPTDVGOAEATRKAAARMW 220
Db 194 HEAMWLRMVELNLGLFLPLAAILFNCILASLRGRGVRVSRGCGPRDSKSTA-LIL 252

QY 221 ANLLVFFVCFPLHVLGLTVRL-----AVGNACALLETIRRALYITSKLSDANCLDAICY 275
Db 253 TLVASFLVCWAPYHFFAPFLECLMQVHAIG--GCFWEEPTDLGLQLSNFSAFVNSCLNPVI 310

QY 276 YTYMAKEP-----QEASALAVAPRAKAKSHQ 301
Db 311 YFVVGRLFRTKVWELCQCQSPRSALAPVSSSRKE 344

Search completed: February 9, 2006, 01:01:14
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Mon Feb 13 13:14:00 2006

us-10-083-168-16.rpr

Page 7

Job time : 28.5 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 00:55:13 ; Search time 26.5 Seconds
(without alignments)
1121.924 Million cell updates

Title: US-10-083-168-85

Perfect score: 1615
Sequence: 1 MNGTYNTCGSSDLTWPPAIK.....AVAPRAKAKHSQDSLCVTILA 309

Scoring table: BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR 80:*

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1: pir1:
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2: pir2:4

3: pir3:4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	400	24.8	370	2	JC5549	heptahelical P2V5-
2	369.5	22.9	387	2	I69202	G protein-coupled
3	367.5	22.8	308	2	I50241	G protein-coupled
4	359.5	22.3	344	2	T09508	intron 17 purinery
5	317	19.6	373	2	A47556	ATP receptor P2u -
6	316	19.6	362	2	S33733	G protein-coupled
7	315.5	19.5	365	2	S68679	G protein-coupled
8	314	19.4	328	2	I55450	G protein-coupled
9	311.5	19.3	354	2	I53033	G protein-coupled
10	311.5	19.3	362	2	A57641	G protein-coupled
11	311.5	19.3	364	2	JQ1488	bradykinin B2 rece
12	311.5	19.3	366	1	OOR782	bradykinin recepto
13	309	19.1	342	2	S13638	platelet-activatin
14	308.5	19.1	362	2	B57841	G protein-coupled
15	307.5	19.0	362	2	S68207	G protein-coupled
16	306.5	19.0	375	2	A54946	P-2U nucleotide re
17	303	18.8	342	2	A40191	platelet-activatin
18	303	18.8	352	2	S60024	bradykinin B1 rece
19	300.5	18.6	373	2	JC4162	P2Y receptor - bo
20	296.5	18.4	373	2	JC4737	G protein-coupled
21	292	18.1	341	2	JC3252	platelet-activatin
22	288	17.8	363	2	JC2543	angiotensin II rec
23	286.5	17.7	352	2	A43113	chemokine (C-C) re
24	286	17.7	328	2	JC4800	P2Y6 receptor - hu
25	284.5	17.6	361	2	B45680	G protein-coupled
26	282	17.5	341	2	S63666	platelet activatin
27	280.5	17.4	366	2	I49519	bradykinin B2 rece
28	279.5	17.3	361	2	JC5653	G protein-coupled
29	278.5	17.2	363	2	I57955	somatostatin recep

30	278.5	17.2	364	2	JN0763	somatostatin recep
31	277	17.2	363	2	A49032	angiotensin II rec
32	274	17.0	363	2	I48261	angiotensin II rec
33	274	17.0	363	2	I57940	somatostatin recep
34	272.5	16.9	365	2	S88208	G protein-coupled
35	270.5	16.7	355	2	I49339	macrophage inflam
36	270.5	16.7	420	2	I51657	thrombin receptor
37	269	16.7	354	2	T09333	G protein-coupled
38	267	16.5	323	1	Q0BE03	HHRF3 protein - hu
39	267	16.5	418	2	A46246	somatostatin recep
40	264.5	16.4	355	2	JC5067	G protein-coupled
41	261.5	16.2	359	2	JC2134	angiotensin II rec
42	261.5	16.2	369	2	JC5068	G protein-coupled
43	261.5	16.2	391	2	A41795	somatostatin recep
44	261.5	16.2	391	2	C41795	somatostatin recep
45	261.5	16.2	391	2	A39297	somatostatin recep

ALIGNMENTS

RESULT 1

JC5549
 heptahelical P2Y5-like receptor - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
 C:Accession: JC5549
 R:Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.
 Biochem. Biophys. Res. Commun. 236, 106-112, 1997
 A:Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.
 A:Reference number: JC5549; MUID:97368605; PMID:9223435
 A:Accession: JC5549
 A:Molecule type: DNA
 A:Residues: 1-370 <JAN>
 A:Cross-references: UNIPROT:Q99677; UNIPARC:UPI000016A4CA; DDBJ:AF005419; NID:G2240034;
 C:Superfamily: ATP receptor P2u

Query Match	24.8%;	Score 400;	DB 2;	Length 370;
Best Local Similarity	34.0%;	Pred. No. 1.3e-29;		
Matches 105: Conservative	58;	Mismatches 104;	Indels 42;	Gaps 11;

Qy	25	AYIGLVIVIGLLNSIALVWFCRCMOQWTTETRIYMTNLAVADICLLCTLPF-VLHSLR---	8
Db	44	AVYSVWPFILGNTSLSVFCFCRMRSETAIFITNLAVSDLLFVCTLPFKFIYFNHR	10
Qy	82	-DTSDPPLCOLSOGIYLTHRYMSISLTAIAVDRVAVVRHPLRARGLSPROQAAACVL	14
Db	104	WPFQDT-LCKISGTAFLTNIYSGMLFTLCISVDRFIAIVYPRSRITIRTRNSAIVCAGV	16
Qy	141	WLIVIGSLVARWLLGQEGGF-----CFR-----STRHNFNSMEFPLLGFLY	18
Db	163	WILVLSG-----GISASLFSFTNNVNNATTCFEGLSKRWKTYLSKTIIEVVGFI	21
Qy	183	PLAVVVFCSLKVYTAQAQRPPDVGQAEAT-RKAKEMVWANLLVFCVCLPLHVGITVRL	24
Db	216	PLILNVSCSSVWRTL--RKPATLSQIGTKKKVKLKMIVHMAVFCVFPVNSVLFLYA	27
Qy	242	AVGNWAC--ALLETIRRALY-ITSKLSDANCCLDIAICYYYMAKBFQASALAVAPRAKH	29
Db	274	LVRSQLATNCFLERFPAKIWPITLCLATLNCDFPIIYFTLESFQKSFVI-----NAH	32
Qy	299	KSQDSLCVT 307	
Db	328	IRMESLEKT 336	

RESULT 2

169202
G protein-coupled receptor HM74 - human
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: 169202
R:Nomura, H.; Nielsen, B.W.; Matsushima, K.

Int. Immunol. 5, 1239-1249, 1993

A>Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemokine receptor
A/Reference number: I54751; MUID:94092629; PMID:7505609
A/Accession: I69202
A>Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-387 <RES>
A/Cross-references: UNIPROT:P49019; UNIPARC:UPI0000043C3C; GB:D10923; NID:g219866; PIDN:G304383
C/Genetics:
A/Gene: HM74
C/Superfamily: G protein-coupled receptor 4

Query Match 22.9%; Score 369.5; DB 2; Length 387;
Best Local Similarity 35.0%; Pred.No.9.4e-27;
Matches 98; Conservative 45; Mismatches 102; Indels 35; Gaps 12;

QY 27 LGVLLVLGLLNSIALWVFCCRMQQWTETIYNLNLAVALDLCLCTLPFVL-----HSLR 81
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
34 LGLEFIPLGLNGLALWFCFLKSKWSKRIFLNLAVALDFLLIICLPFYMDYYVRSDW 93
QY 82 DTSDTPLCQLSQGIYITNRNYSISLVTAIAVDRYAVRHPLRAGRLSPROAAACAVLW 141
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
94 NFGDIP-CRLVLFPANRGSSIFLTVAVDRIYFRVHPHHALKINSWTAIIISCLW 152
QY 142 VLVIG---SILVARWLIGIQSG--GFCEP-STRINP--NSMRFFELGFLYLPLHVGVTLRVLAGW---- 245
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
153 GITVGLTVHLKKKL-LQGPANVCISPSICTHRWEAMF-LLEFLLPLGLIILFCSAR 210
QY 194 VTVALAQRPFDVGQAEATKAKR---MWANLLVFVCFPLPHVGLTVRLAVGW---- 245
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
211 IIWSLRQR-----QMDRHAKIKRAITFMVAIVFVICFLP---SVVVRIRIFWLLHTS 261
QY 246 --NACALLETIRRALYITSKLSDANCCLDAICYVMKEF 283
Db 262 GTONCEVRSVDLAFITLSFTYMNSMLDPVVYFSFSPS 301

RESULT 3
I50241
G protein-coupled receptor 6H1 - chicken
N/Alternate names: purinoceptor 6H1
C/Species: Gallus gallus (chicken)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: I50241; Jc4618
R/Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A/title: Identification of a G protein coupled receptor induced in activated T cells.
A/Reference number: I50241; MUID:93329058; PMID:8393036
A/Accession: I50241
A>Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-308 <KAP>
A/Cross-references: UNIPROT:P32250; UNIPARC:UPI0000055A6B; GB:L06109; NID:g304383; PIDN:G304383
R/Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A/title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A/Reference number: Jc4618; MUID:96190677; PMID:8619790
A/Accession: Jc4618
A/Molecule type: mRNA
A/Residues: 1-308 <WEB>
A/Cross-references: UNIPARC:UPI0000055A6B; GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:G304383
A/Experimental source: T-cells
C/Comment: This receptor plays a role in T-cell activation.
C/Genetics:
A/Gene: p2y5
C/Superfamily: ATP receptor P2u
C/Keywords: G protein-coupled receptor; transmembrane protein
F/15-40/Domain: transmembrane #status predicted <TM1>
F/51-74/Domain: transmembrane #status predicted <TM2>
F/89-109/Domain: transmembrane #status predicted <TM3>
F/133-153/Domain: transmembrane #status predicted <TM4>
F/177-201/Domain: transmembrane #status predicted <TM5>
F/227-248/Domain: transmembrane #status predicted <TM6>

Db 294 TSDTIQNS 301

RESULT 5

A47556

ATP receptor p2u - mouse

C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: A47556

R;Lustig, K.D.; Shiao, A.K.; Brake, A.J.; Julius, D.

Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993

A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.

A;Reference number: A47556; MUID:93281707; PMID:7685114

A;Accession: A47556

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-373 <LUS>

A;Cross-references: UNIPROT:P35383; UNIPARC:UPI0000027DFF; GB:L14751; NID:g309457; PIDN:

C;Superfamily: ATP receptor P2u

C;Keywords: transmembrane protein

Query Match 19.6%; Score 317; DB 2; Length 373;

Best Local Similarity 30.1%; Pred. No. 7.1e-22;

Matches 101; Conservative 54; Mismatches 130; Indels 50; Gaps 11;

Qy 2 NGTYNTCGSSDLTWPPAIKLG- - - - -YAVL- - - - -GVLLVGLLLNSLALWVCCR 48

Db 9 NSTINGTWEGD- - - - -ELGYKCRFNEDEKYVLLPSYGVVGLGLCLNVALYIFLCR 61

Qy 49 MQQTETRIYMTNLAVADLCCLCTLPFVLSLRDTSDF- - - - -YAVL- - - - -GVLLVGLLLNSLALWVCCR 104

Db 62 LKTNASTYIMPHLAVSDLSYAAFLPLLVYVYARGDHPFSTVLCVLRFLFYNYLNCYSI 121

Qy 105 SLVTAIAVDVAVVAVRHPRLARGSLRSPQAAAVCAVLVWLVIGSLVARWLLGIQGGFCFR 164

Db 122 LFLTCISVHRCGLVLRPLHSLRWGRVARRVAAVWVVLV-ACQAPVLYFVTTSVRGTR 180

Qy 165 STRIN- - - - -FNSMRPPLGFLYPLAVVFCVSLKVVTAQAORPP- - - - -TDVGOAE 210

Db 181 ITCHDTSARELFHSFVAYSSVMGLGL-FAVPFSVLVCVLMARLL- - - - -KPAYGTTGGULP 238

Qy 211 ATRKAKRMWANLLVFVFCFLPHVGLTVRLAVGN- - - - -NACALLETIRALYITSKLSDAN 268

Db 239 AKRKSVRTIALVAVFALCFPLFPFHTVTRTYYSFRSLDLSCHTLNAINWAYKIITRPLASAN 298

Qy 269 CCLDAICVY- - - - -NAKEFOEASALAVAPRAK 296

Db 299 SCLDPVLIFLAGQRLVRFARDAKPTEPTSPQAR 333

RESULT 6

S33733

G protein-coupled receptor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: S33733

R;Webb, T.E.; Simon, J.; Krishnak, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock

FEBS Lett. 324, 219-225, 1993

A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.

A;Reference number: S33733; MUID:93285340; PMID:8508924

A;Accession: S33733

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-362 <WEB>

A;Cross-references: UNIPROT:P34996; UNIPARC:UPI00000405D4; EMBL:X73268; NID:g395084; PID

C;Superfamily: ATP receptor P2u

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.6%; Score 316; DB 2; Length 362;

Best Local Similarity 28.2%; Pred. No. 8.5e-22;

Matches 96; Conservative 63; Mismatches 134; Indels 48; Gaps 12;

Qy 1 MNGTY- - - - -NTCGSSDLTWPPAIKLG- - - - -YAVLGVLLV- - - - -GLLLNSLALWV 44

Db 10 LNTQPELLAGWAGNATTKCSLT- - - - -KTGFQFVLTPTVYILVITFGFLGNSVAIWM 64

Qy 45 FCCRMQQTETRIYMTNLAVADLCCLCTLPFVLSLRDTSDF- - - - -TPLCOLSQGIYLTNR 100

Db 65 FVFHMRPWSGISVYMFNLALADFLVLTLPALIFYFNKTDWIFGDMVCKLQRFIFHVN 124

Qy 101 YMSISLVTAIAVDVAVVAVRHPRLARGSLRSPQAAAVCAVLVWLVIGSLVARWLL- - - - -GI 156

Db 125 YGSILFELTCISVRYTVGVHPLKSLGKKNNAVYVSSLVWALV- - - - -AVIAPILFYSQTV 183

Qy 157 QEGG- - - - -FCFSTRHNF- - - - -NSMRPPLGFLYPLAVVFCVSLKVVTAQAORPPTDVGO 208

Db 184 RNKNTITCYDTTADVYLSYFVYVSMCTVFMFCIPFIVILGCGYLIIVLYK- - - - -DLDN 240

Qy 209 AEATRKAKRMWANLLVFVFCFLPHVGLTVRLAVGN- - - - -ACALLETIRALYITSK 263

Db 241 SPLRRKSIYLVILVTVFAVSILYFPHVMKTLNLRDLDFQTPQMCADFNDKVYATYQVTRG 300

Qy 264 LSDANCCCLDAICVYMAKBFQEASALAVAPRAKAKHSQDSL 304

Db 301 LASLNSCVDPILYFLAGDTTFR- - - - -RLSRATRKSSRSEPNV 339

RESULT 7

S68679

G protein-coupled receptor - human

C;Species: Homo sapiens (man)

C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C;Accession: S68679

R;Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.

FEBS Lett. 384, 260-264, 1996

A;Title: Molecular cloning and characterization of a novel orphan receptor (P(2P)) expro

A;Reference number: S68679; MUID:96197801; PMID:8617367

A;Accession: S68679

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-365 <STA>

A;Cross-references: UNIPROT:P51582; UNIPARC:UPI000002E776; EMBL:X96597; NID:g1296631; PI

C;Superfamily: ATP receptor P2u

C;Keywords: G protein-coupled receptor

Query Match 19.5%; Score 315.5; DB 2; Length 365;

Best Local Similarity 29.2%; Pred. No. 9.6e-22;

Matches 94; Conservative 56; Mismatches 123; Indels 49; Gaps 12;

Qy 29 VLLVGLLLNSLALWVFCRMQQTETRIYMTNLAVADLCCLCTLPFVLSLRDTSDF- 87

Db 44 VVFLVGLGLNAPTLMFLRPMWDATATYMFHLALSDTLVLSLPTLIYYAAHNHWP 103

Qy 88 - - - - -LCQLSQGIYLTNYMSISLVTAIAVDVAVVAVRHPRLARGSLRSPQAAAVCAVLWLV 144

Db 104 GTEICKFVRFLFYWNLYCSVLFLTCISVHRYLIGICHLRLRWGRPLAGLCLAVLVV 163

Qy 145 IGSILVAR- - - - -WLLGIQGG- - - - -FCFSTR- - - - -H- - - - -NFNSMRPPLGFLYPLAVVFCVSLK 193

Db 164 AGCLVPNLFFVTTSNGTIVLCHDTRPEEPDHYVHFSSAVMGLL- - - - -FGVPCLVLTVCYGL 222

Qy 194 VVTAQAORPPTDVGOAEATRKAK- - - - -RMVWVANLLVFVFCFLPHVGLTV- - - - -RLAVGWA 247

Db 223 MARRLYQLP- - - - -GSAQSSRLSLRTIAVLTVPVAVCFVPPHITRTIYLLARLLEA- - - - -D 277

Qy 248 CALLETIRALYITSKLSDANCCCLDAICVYMAKBFQE- - - - -ASALAV 291

Db 278 CRVLNIVNVVYKVTPLASANSCLDPVLVLLTGDKYRRLQLRQLCGGKGPQPRTAASSLAL 337

Qy 292 APRAK- - - - -AHKSQDSLQVT 307

Db 338 VSLPEDSSCRWAATPDSSCST 359

RESULT 8

A;Reference number: JH0712; MUID:93038601; PMID:1329734
A;Accession: JH0712
A;Molecule type: DNA
A;Residues: 1-364 <EGG>
A;Cross-references: UNIPROT:P30411; UNIPARC:UPI000002A4FC; GB:S45489; NID:9256536; PIDN:R;Powell, S.J.; Glynn, G.; Thomas, C.; Hopkins, B.; Briggs, I.; Graham, A.
Genomics 15, 435-438, 1993
A;Title: Human bradykinin B2 receptor; nucleotide sequence analysis and assignment to chromosome 15, 435-438, 1993
A;Reference number: A46022; MUID:93194199; PMID:7916737
A;Accession: A46022
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-364 <POW>
A;Cross-references: UNIPARC:UPI000002A4FC; GB:S56772; NID:q298604; PIDN:AAB25765.1; PID:R;Ma, J.; Wang, D.; Ward, D.C.; Chen, L.; Deesal, T.; Chao, J.; Chao, L.
Genomics 23, 362-369, 1994
A;Title: Structure and chromosomal localization of the gene (BDRB2) encoding human bradykinin receptor type B-2 - rat
A;Reference number: A55559; MUID:95137582; PMID:7835885
A;Accession: A55559
A;Molecule type: DNA
A;Residues: 1-364 <MAA>
A;Cross-references: UNIPARC:UPI000002A4FC; GB:L27594
R;Hees, J.P.; Borkowski, J.A.; Young, G.S.; Strader, C.D.; Ransom, R.W.
Biochem. Biophys. Res. Commun. 184, 260-268, 1992
A;Title: Cloning and pharmacological characterization of a human bradykinin (BK-2) receptor
A;Reference number: JQ1488; MUID:92231936; PMID:1314587
A;Accession: JQ1488
A;Molecule type: mRNA
A;Residues: 1-364 <HES>
A;Cross-references: UNIPARC:UPI000002A4FC; GB:M88714; NID:g1387999; PIDN:AAB02793.1; PID:R;Wang, D.; Ma, J.; Chao, L.; Chao, J.
C;Genetics:
A;Gene: GDB:BDRB2
A;Cross-references: GDB:135713; OMIM:113503
A;Map position: 14q32.1-14q32.2
A;Introns: #status absent
A;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;34-56/Domain: transmembrane #status predicted <TM1>
F;66-92/Domain: transmembrane #status predicted <TM2>
F;104-127/Domain: transmembrane #status predicted <TM3>
F;148-171/Domain: transmembrane #status predicted <TM4>
F;195-221/Domain: transmembrane #status predicted <TM5>
F;241-266/Domain: transmembrane #status predicted <TM6>
F;285-309/Domain: transmembrane #status predicted <TM7>
F;312,180/Binding site: carboxylate (Thr) (covalent) #status predicted
F;170,237,342/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
F;242/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
F;316/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 19.3%; Score 311.5; DB 2; Length 364;
Best Local Similarity 27.6%; Pred. No. 2.3e-21;
Matches 89; Conservative 54; Mismatches 128; Indels 51; Gaps 9;

Qy 1 MNGTYTCGSSDLTW-----PPAIGLGFAYGLVGLVGLLNLALWVFCRCMQQW 52
Db 11 LNTGTPAQSKCPQVGLWNLTIQPP-----FLWLVFLVLALENIFVLSVFCVLUHKKSC 62

Qy 53 TETRITMTNLAVADLCCLCTLPFVLHSLRDTSD-----TPICQLSQGIVLTNRYMSISLVT 108
Db 63 TVAEIYLGNAADLIACGLFPFWAITISNNFDLPGETLCRVNVAIISMLYSSICFLM 122

Qy 109 AIADRYVAVRHPLRARGLSRQAACVAVLW--VLVIGS--LVARWLLGIQEGGFCFR 164
Db 123 LVSDRYLALVKTMSGMRGVRAKLYSLVINGCTLLSSPMLVFTWKEYSDREG---- 178

Qy 165 STRHN-----FNSMRFPFLGFLPLAVVFCSLKVVVTAALAQRPPTDVGOA 209
Db 179 ---HNVTACVISPSLIWEVFTMLNLNVGFLPLSVITFTCTVIMQVLRNNEKFKVEIK 235

Qy 210 EATRAKAKMVAANTLVFVVCPLPLHVLTV----LVAGWNAALLETIRRALYITSKLS 265
Db 236 QTERATVTLVVLVLLFIICWLPFQISFTDLTLRLGI--LSSCQDERIIDVITQIASFWA 294

Qy 266 DANCCCLDAICYYYMAKEFOEAS 287
Db 295 YSNSCLNPLVYIVGKRFRKKS 316

RESULT 12

COORTB2
bradykinin receptor type B-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A41283; A55079; S47529
R;McEachern, A.E.; Shelton, E.R.; Bhakta, S.; Obermole, R.; Bach, C.; Zuppan, P.; Fujis
Proc. Natl. Acad. Sci. U.S.A. 88, 7724-7728, 1991
A;Title: Expression cloning of a rat B-2 bradykinin receptor.
A;Reference number: A41283; MUID:91352062; PMID:1715575
A;Accession: A41283
A;Molecule type: mRNA
A;Residues: 1-366 <MCE>
A;Cross-references: UNIPROT:P25023; UNIPARC:UPI00001708A1; GB:M59967
R;Pesquero, J.B.; Lindsey, C.J.; Zeh, K.; Paiva, A.C.M.; Ganten, D.; Bader, M.
J. Biol. Chem. 269, 26920-26925, 1994
A;Title: Molecular structure and expression of rat bradykinin B2 receptor gene. Evidence
A;Reference number: A55079; MUID:95014558; PMID:7929432
A;Accession: A55079
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-75, 'A', 77-366 <PES>
A;Cross-references: UNIPARC:UPI000002A4FE; GB:X80187; GB:X80188; GB:X80189; GB:X80190
R;Wang, D.; Ma, J.; Chao, L.; Chao, J.
Biochim. Biophys. Acta 1219, 171-174, 1994
A;Title: Molecular cloning and sequence analysis of rat bradykinin B(2) receptor gene.
A;Reference number: S47529; MUID:94368850; PMID:8086459
A;Accession: S47529
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-366 <WAN>
A;Cross-references: UNIPARC:UPI00001708A1; EMBL:L26173; NID:9476749; PIDN:AAA62492.1; PI
C;Comment: This G protein-coupled receptor binds the nonapeptide bradykinin.
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;
F;31-48/Domain: transmembrane #status predicted <TM1>
F;79-96/Domain: transmembrane #status predicted <TM2>
F;107-126/Domain: transmembrane #status predicted <TM3>
F;154-170/Domain: transmembrane #status predicted <TM4>
F;197-215/Domain: transmembrane #status predicted <TM5>
F;245-261/Domain: transmembrane #status predicted <TM6>
F;312,180/Binding site: carboxylate (Asn) (covalent) #status predicted
F;105-186/Disulfide bonds: #status predicted
F;326/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 19.3%; Score 311.5; DB 1; Length 366;
Best Local Similarity 28.1%; Pred. No. 2.3e-21;
Matches 90; Conservative 54; Mismatches 127; Indels 49; Gaps 9;

Qy 2 NGTYTCGSSDLTWPPAIGLGFAYGLVGLVGLLNLALWVFCRCMQQWTETRIYMTN 61
Db 14 NGTFSEVNCPTDEWWSNLNAIQAPFLVLFLLAALENIFVLSVFCVCLHKTCTVAEIYLG 73

Qy 62 LAVADLCCLCTLPFVLHSLRDTSD-----TPICQLSQGIVLTNRYMSISLVTAIADRYVA 117
Db 74 LAGADLIACGLFPFWAITIANNFDLFGVLCRVVNTMIYNNLYSSICFLMLVSDRYLA 133

Qy 118 VRHPLRARGLSRQAACVAVLW--VLVIGS--LVARWLLGIQEGGFCFRSTRN---- 169
Db 134 LVKTMGMRGVRAKLYSLVINGCTLLSSPMLVFTWKEYSDREG-----HNVTAC 186

Qy 170 -----FNSMRFPFLGFLPLAVVFCSLKVVVTAALAQRPPTDVGOABATRAKEM 218
Db 187 VIVYPSRSEWFTMLNLNVGFLPLSVITFTCTVIMQVLRNNEKFKVEQTEKATVL 246

Qy 219 VVANLLVFCVPLPLHVLTV--LTVRLAVG-----WNAALLETIRRALYITSKLSD----A 267

```
Db      247 VLAIVGLFVLCWFPFQISTDLTLRLGLVSGCWN-----ERAVDIVTQISSVAYS 298
Qy      268 NCCLDAICYYMAKEPQES 287
Db      299 NSCLNPLVYIVGKRFKK 318

RESULT 13
S13638
platelet-activating factor receptor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S13638
R:Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; To
Nature 349, 342-346, 1991
A:Title: Cloning by functional expression of platelet-activating factor receptor from gu
A:Reference number: S13638; MUID:91101726; PMID:1846231
A:Accession: S13638
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-342 <HON>
A:Cross-references: UNIPROT:P1556; UNIPARC:UPI00001311EE; GB:X56736; NID:G49442; PIDN:O
A>Note: the species of guinea pig is not identified; in GenBank entry CCPAPREC, release
C:Superfamily: ATP receptor P2u

Query Match      19.1%; Score 309; DB 2; Length 342;
Best Local Similarity 28.2%; Pred. No. 3.6e-21;
Matches 81; Conservative 58; Mismatches 110; Indels 38; Gaps 9;

Qy      29 VLVLLGLLNSLALWVFCRM---QQTETRIYMTNLAVADLCCLCTLP--FVLHSLRDT 83
Db      24 IIFVLGIANGYVWVP-ARLPFSKLNKIKFVNLTVADLLFLITPLWIVYVYSGN 82

Qy      84 STTP--LCQLSQGIYLTNRYSISLVTATAVDYVAVRHPLRARGLSPROAAACAVLW 141
Db      83 WFLPKPLCNLAGCLFPINTYCVSVAFLGVITVYRNFQAVKYPKTAQATKRGIALSLVW 142

Qy      142 VLVIGSLVARWLLIQE-----GGFCFSTRNFNSMRPPL-----LGFVPLA 185
Db      143 VAIVAA--ASYFLVMDSTNVSNKAGSGNITRCFEHYEKGSRPVLIIHICIVLGFVFL 200

Qy      186 VVVFCSLKVVTALAAQRPPTDVGOAEATRAKAMVWANTLVVFCFLPLHVGTLVRLAVGW 245
Db      201 LILFCNLVLIHLLRQPVKQRAEVRRLMWCTVLAIVVICFVPHM-----VQLPW 255

Qy      246 NACAL-----LETIRRALYITSKLSANDCCCLDAICYYYMAKEPQES 285
Db      256 TLAEGLMWPSSNHQAINDAHQVTLCLLSTNCVLDPVYICFLTKKPK 302

RESULT 14
B57641
G protein-coupled receptor 4 - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C:Accession: B57641
R:Mahadevan, M.S.; Baird, S.; Bailly, J.E.; Shutler, G.G.; Sabourin, L.A.; Tsilfidis, C.
Genomics 30, 84-88, 1995
A:Title: Isolation of a novel G protein-coupled receptor (GPR4) localized to chromosome
A:Reference number: A57641; MUID:96129306; PMID:8595909
A:Accession: B57641
A>Status: preliminary; nucleic acid sequence not shown; translation not shown; significa
A:Molecule type: DNA
A:Residues: 1-362 <MAH>
A:Cross-references: UNIPROT:P50132; UNIPARC:UPI000012BA33; GB:U22108; NID:G722282; PIDN:
C:Genetics:
A:Introns: #status absent
C:Superfamily: G protein-coupled receptor 4
C:Keywords: G protein-coupled receptor

Query Match      19.1%; Score 308.5; DB 2; Length 362;
Best Local Similarity 30.6%; Pred. No. 4.3e-21;
Matches 93; Conservative 48; Mismatches 114; Indels 49; Gaps 11;
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Qy      2 NGTYNTC---GSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRMQOOWTETRIY 58
Db      3 NGTWEGCHVDGRVDHLFPFSL-----YIFVIGV-GLPTNCLRLMAAYRQVRQRELGVY 55

Qy      59 MTNLAVADLCCLCTLP----FVLHSLRDTSDTPLCOLSQGIYLTNRYSISLVTATAVDR 114
Db      56 LNLISADLLYICSLPLWVDYFLHHDNWIHGGSGCKLPGFIYTYNIYISIAFLCCISVDR 115

Qy      115 YVAVRHPLRARGLSPROAAACAVLWLVLVIGS-----LVARWLLGIOEGGFCFRST-RHN 169
Db      116 YLAVAHPLRPLRVRKVTAVAVSSVVMATLGANSVPLFHDEL-----FRDRYNHT 166

Qy      170 FNSMRPPL-----LGFVPLAVVFCSLKVVTALAAQRPPTDVGOAEATRAKAK 216
Db      167 FCFEKKPMEGVAMNLYRVFVGLFPWALMLLSYRGILRAVRGVSST---ERQEKAKIK 223

Qy      217 RMVWANTLVVFCFLPLHVGTLVRLAV---GWNACALLETTIRRALYITSKLSANDCCCLD 272
Db      224 RLALSLIAVLVCFAPYHYVLLSRSAVYLGHFWD-CGFEERVFSAYHSSLAFTSLNCVAD 282

Qy      273 AICY 276
Db      283 PLY 286

RESULT 15
S68207
G protein-coupled receptor 6C.1 - human
C:Species: Homo sapiens (man)
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68207
R:An, S.; Teal, C.; Goetzl, E.J.
FEBS Lett. 375, 121-124, 1995
A:Title: Cloning, sequencing and tissue distribution of two related G protein-coupled re
A:Reference number: S68207; MUID:96087098; PMID:7498459
A:Accession: S68207
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-362 <ANS>
A:Cross-references: UNIPROT:P46093; UNIPARC:UPI000016A24A; EMBL:U35399; NID:G1015420; PIR
C:Superfamily: G protein-coupled receptor 4
C:Keywords: G protein-coupled receptor

Query Match      19.0%; Score 307.5; DB 2; Length 362;
Best Local Similarity 31.0%; Pred. No. 5.3e-21;
Matches 93; Conservative 49; Mismatches 117; Indels 41; Gaps 11;

Qy      2 NGTYNTC---GSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRMQOOWTETRIY 58
Db      3 NHTWEGCHVDGRVDHLFPFSL-----YIFVIGV-GLPTNCLALMAAYRQVRQRELGVY 55

Qy      59 MTNLAVADLCCLCTLP----FVLHSLRDTSDTPLCOLSQGIYLTNRYSISLVTATAVDR 114
Db      56 LNLISADLLYICSLPLWVDYFLHHDNWIHGGSGCKLPGFIYTYNIYISIAFLCCISVDR 115

Qy      115 YVAVRHPLRARGLSPROAAACAVLWLVLVIGSLVARWLLGIOEGGFCFRST-RHNFNM 173
Db      116 YLAVAHPLRPLRVRKVTAVAVSSVVMATLGANSAP--LFHDE---LFRDRYNHTFCFE 170

Qy      174 RPPL-----LGFVPLAVVFCSLKVVTALAAQRPPTDVGOAEATRAKAKRWV 220
Db      171 KFPMEGVAMNLYRVFVGLFPWALMLLSYRGILRAVRGVSST---BRQEKAKIKRAL 227

Qy      221 ANLLVVFVFCFLPLHVGTLVRLAV---GWNACALLETTIRRALYITSKLSANDCCCLDAICY 276
Db      228 SLIAVLVCFAPYHYVLLSRSAIYLGRPWD-CGFEERVFSAYHSSLAFTSLNCVADPLY 286
```

Search completed: February 9, 2006, 01:01:14
Job time : 26.5 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 00:47:43 ; Search time 165 Seconds

(without alignments)
1321.262 Million cell updates/sec

Title: US-10-083-168-85

Perfect score: 1615

Sequence: 1 MNGTYNTCGSSDLTWPPAIAK.....AVAPRAKAHKSQDSLVCVTLA 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1603	99.3	309	Q6FH18_HUMAN	Q6fh18 homo sapien
2	1597	98.9	309	Q6FH18_HUMAN	Q6fh18 homo sapien
3	1597	98.9	309	Q6FH18_HUMAN	Q6fh18 homo sapien
4	1597	98.9	309	Q6FH18_HUMAN	Q6fh18 homo sapien
5	1592	98.6	308	Q6VBN5_HUMAN	Q6vbn5 homo sapien
6	1123	69.5	307	Q6VBN5_HUMAN	Q6vbn5 mus musculus
7	1123	69.5	307	Q6VBN5_HUMAN	Q6vbn5 mus musculus
8	1122	69.5	307	Q6VBN5_HUMAN	Q6vbn5 mus musculus
9	1108	68.6	307	Q6VBN5_HUMAN	Q6vbn5 mus musculus
10	416.5	25.8	305	Q4TAH0_TETNG	Q4tah0 tetraodon n
11	402	24.9	370	Q502U9_HUMAN	Q502u9 homo sapien
12	401	24.8	370	Q502U9_HUMAN	Q502u9 homo sapien
13	399	24.7	370	Q6NSP5_HUMAN	Q6nsp5 homo sapien
14	399	24.7	370	Q6NSP5_HUMAN	Q6nsp5 homo sapien
15	391	24.2	370	Q6BLG2_MOUSE	Q6blk2 mus musculus
16	381.5	23.6	302	Q488W3_TETNG	Q488w3 tetraodon n
17	376.5	23.3	363	Q8TDS4_HUMAN	Q8tds4 homo sapien
18	374	23.2	319	Q6VBN5_HUMAN	Q6vbn5 mus musculus
19	369.5	22.9	387	Q109B4_HUMAN	Q109b4 homo sapien
20	369.5	22.9	387	Q109B4_HUMAN	Q109b4 homo sapien
21	368	22.8	345	Q4RFP7_TETNG	Q4rfp7 tetraodon n
22	367.5	22.8	308	Q2RY5_CHICK	Q2ry5 gallus gall
23	366	22.7	347	Q7Z2A4_BRARE	Q7zza4 brachydanio
24	360.5	22.3	296	Q9WU09_RAT	Q9wu09 rattus norv
25	360.5	22.3	344	Q1RY5_HUMAN	Q1ry5 homo sapien
26	360	22.3	372	Q5K92_HUMAN	Q5k92 homo sapien
27	360	22.3	372	Q5K92_HUMAN	Q5k92 homo sapien
28	356.5	22.1	344	Q2RY5_MOUSE	Q2ry5 mus musculus
29	355	22.0	344	Q4G072_RAT	Q4g072 rattus norv
30	354.5	22.0	344	Q53FA0_HUMAN	Q53fa0 homo sapien
31	348.5	21.6	360	Q9EP66_MOUSE	Q9ep66 mus musculus

RESULT 1

Q6FH18_HUMAN

ID Q6FH18_HUMAN PRELIMINARY; PRT; 309 AA.

AC Q6FH18; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE GPR35 protein.

GN Name=GPR35;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,

RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,

RA Korn B., Zuo D., Hu Y., LaBaer J.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC EMBL; CR541765; CAG46564.1; -; mRNA.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm1.1.

DR PRINTS; PR00237; GPCRHHODPSN.

DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.

DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.

KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.

SEQUENCE 309 AA; 34141 MW; FC034FB7231B26F1 CRC64;

Query Match 99.3%; Score 1603; DB 2; Length 309;

Best Local Similarity 99.4%; Pred. No. 7.1e-112;

Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIAKLGFAVLGVLLGLLNSLALWVFCRCMQQTETRIYMT 60

Db 1 MNGTYNTCGSSDLTWPPAIAKLGFAVLGVLLGLLNSLALWVFCRCMQQTETRIYMT 60

QY 61 NLAVADLCCLCTLPVLSLSDTSLPCLSQGLYLTNRVMSISLVTAIVDRVAVRH 120

Db 61 NLAVADLCCLCTLPVLSLSDTSLPCLSQGLYLTNRVMSISLVTAIVDRVAVRH 120

QY 121 PLRAGLSPQAAACAVLWVLTGSLVARWLLGIOEGGFCFRSTRHNFNSMRPFLG 180

Db 121 PLRAGLSPQAAACAVLWVLTGSLVARWLLGIOEGGFCFRSTRHNFNSMRPFLG 180

QY 181 YLPLAVVFCSLKVVTTALAQRPPTDVGQAEATKAKRMWVWVLCFLPLHVLTVR 240

Db 181 YLPLAVVFCSLKVVTTALAQRPPTDVGQAEATKAKRMWVWVLCFLPLHVLTVR 240

Q4SPQ4_TETNG
Q80239_RAT
Q8VE54_MOUSE
P41232_RAT
P41231_HOMO_SAPIEN
Q4VBN1_HOMO_SAPIEN
Q5XG86_XENOPUS_LAE
Q9BXC0_HOMO_SAPIEN
Q95N03_SUS_SCROFA
Q6P852_XENTR
Q8C131_MUS_MUSCULU
Q35811_RAT
Q4VBB7_HOMO_SAPIEN
Q5YA25_PIG

ALIGNMENTS

QY 241 LAVGNACALLETIRRALYITSKSDANCLDAICYYMAKEFOEASALAVAPRAKAKS 300
 DB 241 LAVGNACALLETIRRALYITSKSDANCLDAICYYMAKEFOEASALAVAPRAKAKS 300
 QY 301 QDSLCVTLA 309
 DB 301 QDSLCVTLA 309

RESULT 2
 GPR35 HUMAN
 ID GPR35 HUMAN STANDARD; PRT; 309 AA.
 AC O9HC97; O43495; O86UR4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Probable G-protein coupled receptor 35.
 GN Name=GPR35;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND VARIANT ARG-294.
 RX MEDLINE=98140132; PubMed=9479505; DOI=10.1006/geno.1998.5095;
 RA O'Dowd B.F., Nguyen T., Marchese A., Cheng R., Lynch K.R.,
 RA Heng H.H.Q., Kolakowski L.F. Jr., George S.R.;
 RT "Discovery of three novel G-protein-coupled receptor genes";
 RL Genomics 47:310-313 (1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE, AND VARIANTS THR-25; ILE-29; MET-108; SER-125 AND
 RP MET-253.
 RX MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;
 RA Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,
 RA Hinokio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,
 RA del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Collilla S.,
 RA Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,
 RA Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
 RA Bell G.I.;
 RT "Genetic variation in the gene encoding calpain-10 is associated with
 RT type 2 diabetes mellitus";
 RL Nat. Genet. 26:163-175 (2000).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RA Warren C.N., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Orphan receptor.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in all adult and fetal tissues
 CC examined, including pancreatic islets and skeletal muscle, with
 CC relatively higher levels in adult lung, small intestine, colon and
 CC stomach.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

EMBL; AF027957; AAC52028.1; -; Genomic DNA.
 EMBL; AF089087; AAG17965.1; -; mRNA.
 EMBL; AY275467; AAP32299.1; -; Genomic DNA.
 Ensembl; ENSG00000178623; Homo sapiens.
 HGNC; HGNC:4492; GPR35.
 MIM; 602646; -.
 GO; GO:0005887; C:integral to plasma membrane; TAS.
 GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
 GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
 InterPro; IPR00276; GPCR_Rhodopsin.

Pfam; PF00001; 7tm 1; 1.
 PRINTS; PR00237; GPCRHOOPS.
 PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Glycoprotein; Polymorphism; Receptor;
 KW Transducer; Transmembrane.
 FT TOPO_DOM 1 24 Extracellular (Potential).
 FT TRANSMEM 25 45 1 (Potential).
 FT TOPO_DOM 46 56 Cytoplasmic (Potential).
 FT TRANSMEM 57 77 2 (Potential).
 FT TOPO_DOM 78 90 Extracellular (Potential).
 FT TRANSMEM 91 112 3 (Potential).
 FT TOPO_DOM 113 135 Cytoplasmic (Potential).
 FT TRANSMEM 136 156 4 (Potential).
 FT TOPO_DOM 157 174 Extracellular (Potential).
 FT TRANSMEM 175 195 5 (Potential).
 FT TOPO_DOM 196 218 Cytoplasmic (Potential).
 FT TRANSMEM 219 239 6 (Potential).
 FT TOPO_DOM 240 258 Extracellular (Potential).
 FT TRANSMEM 259 279 7 (Potential).
 FT TOPO_DOM 280 309 Cytoplasmic (Potential).
 FT CARBOHYD 2 2 N-linked (GlcNAc...) (Potential).
 FT DISULFID 89 162 By similarity.
 FT VARIANT 25 25 A->T.
 FT VARIANT 29 29 /FTID=VAR_013601.
 FT VARIANT 108 108 /FTID=VAR_013602.
 FT VARIANT 125 125 /FTID=VAR_013603.
 FT VARIANT 253 253 /FTID=VAR_013604.
 FT VARIANT 294 294 /FTID=VAR_013605.
 FT CONFLICT 174 174 A->R (in Ref. 1).
 SQ SEQUENCE 309 AA; 34072 MW; 97734PB7231B26F0 CRC64;
 Query Match 98.9%; Score 1597; DB 1; Length 309;
 Best Local Similarity 99.0%; Pred. NO. 2e-111;
 Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MNGYNTCGSSDLTPWPPAIIKLGYPAYLGVLVIGLLNSLALWVFCRMOQTETRIYMT 60
 DB 1 MNGYNTCGSSDLTPWPPAIIKLGYPAYLGVLVIGLLNSLALWVFCRMOQTETRIYMT 60
 QY 61 NLAVADLCCLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTAIVDRVAVRH 120
 DB 61 NLAVADLCCLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTAIVDRVAVRH 120
 QY 121 PLRARGLSRQAAAVCAVLAQRPPTDVGQAEATRAKRMVWNLVVFVCFPLHVLTVR 180
 DB 121 PLRARGLSRQAAAVCAVLAQRPPTDVGQAEATRAKRMVWNLVVFVCFPLHVLTVR 180
 QY 181 YLPLAVVVFCSIKVVTALAQRPTDVGQAEATRAKRMVWNLVVFVCFPLHVLTVR 240
 DB 181 YLPLAVVVFCSIKVVTALAQRPTDVGQAEATRAKRMVWNLVVFVCFPLHVLTVR 240
 QY 241 LAVGNACALLETIRRALYITSKSDANCLDAICYYMAKEFOEASALAVAPRAKAKS 300
 DB 241 LAVGNACALLETIRRALYITSKSDANCLDAICYYMAKEFOEASALAVAPRAKAKS 300
 QY 301 QDSLCVTLA 309
 DB 301 QDSLCVTLA 309

RESULT 3
 Q42FV2 HUMAN
 ID Q42FV2 HUMAN PRELIMINARY; PRT; 309 AA.
 AC Q42FV2
 DT 13-SEP-2005 (TRENBLrel. 31, Created)
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)

```

DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
OS Hypothetical protein FLJ16773.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saio K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AK131540; BAD18676.1; -; mRNA.
DR Ensembl; ENSG00000178623; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
DR KW G-protein coupled receptor; Hypothetical protein; Receptor;
KW Transducer; Transmembrane.
SQ SEQUENCE 394 AA; 43309 MW; 1598FD44BAE4233C CRC64;

Query Match 98.9%; Score 1597; DB 2; Length 394;
Best Local Similarity 99.0%; Pred. No. 2.5e-111;
Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPPAIKLGFYALGVLLVGLLNSLALWVFCRMOQWTTETRIYMT 60
DB 86 MNGTYNTCGSSDLTPPAIKLGFYALGVLLVGLLNSLALWVFCRMOQWTTETRIYMT 145

QY 61 NLAVADICLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDYVAVRH 120
DB 146 NLAVADICLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDYVAVRH 205

QY 121 PLRAGLRSRQAAAVCAVAVLVIGSLVARWLLGIQEGGFCFRSTRNFNSMFPLLGF 180
DB 206 PLRAGLRSRQAAAVCAVAVLVIGSLVARWLLGIQEGGFCFRSTRNFNSMFPLLGF 265

QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRAKRWANLVVFCFLPLHVLTVR 240
DB 266 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRAKRWANLVVFCFLPLHVLTVR 325

QY 241 LAVGNACALLETIRRALYITSKLSANDCCLDALCIYYTMAKEFOEASALAVAPRAKAHS 300
DB 326 LAVGNACALLETIRRALYITSKLSANDCCLDALCIYYTMAKEFOEASALAVAPRAKAHS 385

QY 301 QDSLCTVLA 309
DB 386 QDSLCTVLA 394

RESULT 5
Q4VENS HUMAN PRELIMINARY; PRT; 308 AA.
ID Q4VENS5
AC Q4VENS5
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE GPR35 protein (Fragment).
GN Name=GPR35;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
OS Hypothetical protein GPR35.
GN Name=GPR35;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Haakenson W., Trani L., Schatzkammer K.;
RA "The sequence of Homo sapiens BAC clone RP11-27M15."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AC124862; AAX88945.1; -; Genomic_DNA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
DR KW G-protein coupled receptor; Hypothetical protein; Receptor;
KW Transducer; Transmembrane.
SQ SEQUENCE 309 AA; 34072 MW; 97734FB7231B26F0 CRC64;

Query Match 98.9%; Score 1597; DB 2; Length 309;
Best Local Similarity 99.0%; Pred. No. 2e-111;
Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPPAIKLGFYALGVLLVGLLNSLALWVFCRMOQWTTETRIYMT 60
DB 1 MNGTYNTCGSSDLTPPAIKLGFYALGVLLVGLLNSLALWVFCRMOQWTTETRIYMT 60

QY 61 NLAVADICLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDYVAVRH 120
DB 61 NLAVADICLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDYVAVRH 120

QY 121 PLRAGLRSRQAAAVCAVAVLVIGSLVARWLLGIQEGGFCFRSTRNFNSMFPLLGF 180
DB 121 PLRAGLRSRQAAAVCAVAVLVIGSLVARWLLGIQEGGFCFRSTRNFNSMFPLLGF 180

QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRAKRWANLVVFCFLPLHVLTVR 240
DB 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRAKRWANLVVFCFLPLHVLTVR 240

QY 241 LAVGNACALLETIRRALYITSKLSANDCCLDALCIYYTMAKEFOEASALAVAPRAKAHS 300
DB 241 LAVGNACALLETIRRALYITSKLSANDCCLDALCIYYTMAKEFOEASALAVAPRAKAHS 300

QY 301 QDSLCTVLA 309
DB 301 QDSLCTVLA 309

RESULT 4
Q6ZMP9 HUMAN PRELIMINARY; PRT; 394 AA.
ID Q6ZMP9
AC Q6ZMP9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
```

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 RN NCBI_TaxID=9606;
 RN [1]
 RC TISSUE=G-protein coupled receptors;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zerborg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=G-protein coupled receptors;
 RG NIH MGC Project;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 DR EMBL; BC095500; AAH95500.1; -; mRNA.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
 DR PROSITE; PS00262; G PROTEIN RECP F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 FT NON_TER 1
 FT NON_TER 308
 SQ SEQUENCE 308 AA; 33941 MW; 5791BF9CE7206034 CRC64;
 Query Match 98.6%; Score 1592; DB 2; Length 308;
 Best Local Similarity 99.0%; Pred. No. 4.7e-111;
 Matches 305; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 NGTYNTCGSDLTWPPAIIKGLFYAYLVGLVLLGLLNSLALWVFCRMOQWETRIYMTN 61
 Db 1 NGTYNTCGSDLTWPPAIIKGLFYAYLVGLVLLGLLNSLALWVFCRMOQWETRIYMTN 60
 QY 62 LAVADICLLCTLPFVLHSLRDTSDTLPCLQSQGIYLTNRYMSISLTAIVORYVAVRHP 121
 Db 61 LAVADICLLCTLPFVLHSLRDTSDTLPCLQSQGIYLTNRYMSISLTAIVORYVAVRHP 120
 QY 122 LRARGLSRQRAAACAVALWLVIGSLVARWLLGIQGGFCFSTRHNFNSRFPFLIGFY 181
 Db 121 LRARGLSRQRAAACAVALWLVIGSLVARWLLGIQGGFCFSTRHNFNSRFPFLIGFY 180
 QY 182 LPLAVVVFCSLKVVTAALQRPPTDVGQABATRAKRWANLVFVVCFLPLHVLGTVRL 241
 Db 181 LPLAVVVFCSLKVVTAALQRPPTDVGQABATRAKRWANLVFVVCFLPLHVLGTVRL 240
 QY 242 AVGNWACALLETIRRALYITSLSDANCCCLDAICYYYMAKEFOESALAVAPAKAHKQ 301
 Db 241 AVGNWACALLETIRRALYITSLSDANCCCLDAICYYYMAKEFOESALAVAPAKAHKQ 300
 QY 302 DSLCVTLA 309
 Db 301 DSLCVTLA 308

RESULT 6
 GPR35_MOUSE
 ID GPR35_MOUSE STANDARD; PRT; 307 AA.
 AC Q9ES90;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Probable G-protein coupled receptor 35.
 GN Name=Gpr35;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;
 RA Horioka Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,
 RA Hinokio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,
 RA del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla S.,
 RA Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,
 RA Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
 RA Bell G.I.,
 RT "Genetic variation in the gene encoding calpain-10 is associated with
 RT type 2 diabetes mellitus.";
 RL Nat. Genet. 26:163-175 (2000).
 RN [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zerborg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Orphan receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; AF200349; AAG18487.1; -; mRNA.
 CC EMBL; BC027429; AAH27429.1; -; mRNA.
 CC Ensemble; ENSMUSG00000026271; Mus musculus.
 CC MGI; MGI:1929509; Gpr35.
 CC GO; GO:0016021; C: integral to membrane; TAS.
 CC InterPro; IPR000276; GPCR_Rhodopsin.
 CC InterPro; IPR002286; P2_purinocptor.
 CC Pfam; PF00001; 7tm1; 1.
 CC PRINTS; PR00237; GPCRHOPOPSN.
 CC PROSITE; PR01157; P2Y_PURINOCPTOR.
 CC PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
 CC PROSITE; PS00262; G PROTEIN RECP F1_2; 1.

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 Wyznawski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 Hayashizaki Y.,
 "Functional annotation of a full-length mouse cDNA collection.";
 Nature 409:685-690(2001).
 [3]
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Bone;
 The FANTOM Consortium,
 "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 Nature 420:563-573(2002).
 [4]
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Bone;
 MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 Genome Res. 10:1617-1630(2000).
 [5]
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Bone;
 MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 Konno H., Akiyama J., Nishi K., Kitsuaki T., Tashiro H., Itoh M.,
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
 Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 Genome Res. 10:1757-1771(2000).
 [6]
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Bone;
 Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 Nishi K., Nomura K., Nunazaki R., Ohno M., Ohsato N., Okazaki Y.,
 Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 EMBL; AK036503; BAC29453.1; -; mRNA.
 DR MG1; MG1:1929509; Gpr35.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR000276; GPCR Rhodopsin.
 DR InterPro; IPR002286; P2_purnocptor.
 Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR002137; GPCRHHODPSN.
 DR PRINTS; PR01157; P2YFURNOCPTR.
 DR PROSITE; PS00337; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS02622; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 307 AA; 34140 MW; 8EB439A9ED5P7656 CRC64;
 Query Match 69.5%; Score 1122; DB 2; Length 307;
 Best Local Similarity 71.9%; Pred. No. 6.2e-76;
 Matches 223; Conservative 30; Mismatches 51; Indels 6; Gaps 5;
 QY 1 MNGTYNTGSSDLTPWPAKLGAYLVGLVLLVGLLLNSLALWVFCRMOQWTTETRIYMT 60
 DB 1 MNST--TCNST-LTWPAVNVNFTTYSALLVGLLLNSVALWVFCYRQHWQMTETRIYMT 57
 QY 61 NLAVADLCCLCTLPFLVLSLR-DTSDTPLCQLSQGIYLTNRYSISLVTAIVDRYVAVR 119
 DB 58 NLAVADLCCLCSLPFLVLSKYSSDTPVQQLSQGIYLTNRYSISLVTAIVDRYVAVR 117
 QY 120 HPLRARGLRSPQAAAVCAVLVVLVGLSVARWLGIQSGGFCPRS-TRHNFSNMRFPPLL 178
 DB 118 HPLRARELRSPQAAAVCAVLVVLVGLSVARWLGMQSGGFCFSQTERNFSTTAFSL 177
 QY 179 GPYLPVAVVFCSLKVVLTALQRPPTDVQQAETKAKEMVWNLVVFVVCFLPLHVGIT 238
 DB 178 GPYLPVAVVFCSLQVTVLSRPAADVQQAETKATHTMWNANLAVFVICFLPLHVL 237
 QY 239 VRLAVGNACALLETIRALYITSKLSDANCCDAICYYTMAKFEQASALAVAPRAKAH 298
 DB 238 VQVSLNLTCAARDTPSRALSITGKLSDTNCCDAICYYTMAKFEQASKPATSSNT-PH 296
 QY 299 KSQDSLCVTL 308
 DB 297 KSQDSQILSL 306
 RESULT 9
 QBBS98 MOUSE
 ID QBBS98_MOUSE PRELIMINARY; PRT; 307 AA.
 AC QBBS98;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 12 days embryo embryonic body between diaphragm region
 DE and neck cDNA, RIKEN full-length enriched library, clone:9430051l15
 DE product:G protein-coupled receptor 35, full insert sequence.
 GN Name=Gpr35;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RC TISSUE=Embryonic body between diaphragm region and neck;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RC TISSUE=Embryonic body between diaphragm region and neck;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayaishizaki Y.;
RA "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura H., Hahama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayaishizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384 format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hasehizume W.,
RA Hayaishida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Horii P., Imorani K., Iehii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi P., Takaku-Akaiura S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayaishizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AK034870; BAC28861.1; -; mRNA.
DR MGI; MGI:1929509; Gpr35.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR002286; P2_purinocpt.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_HODOPSN.
DR PRINTS; PR01157; P2PURONOPT.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 307 AA; 34260 MW; 923D02CECB0D70AC CRC64;
Query Match 58.6%; Score 1108; DB 2; Length 307;
Best Local Similarity 71.3%; Pred. No. 6.9e-75;
Matches 221; Conservative 30; Mismatches 53; Indels 6; Gaps 5;
QY 1 MNGTYNTGSSDLTWPPAIGKFGYAVLGVLLVGLLNSLALWVFCRMOQMTETRIYMT 60
DB 1 MNST--TCNST--LTWPASVNNPFIYSALLVGLLNSVALWVFCVHQMTETRIYMT 57
QY 61 NLAVALDCLLCTLPFVLSLR-DTSTPLCQLSQGIYLTNRYMSISLVTAIVDRYAVR 119
DB 58 NLAVALDCLLCSLPFVLSLYKSSDTPVCSQGIYLTNRYMSISLVTAIVDRYAVR 117
QY 120 HPLRARGLSRPROAAAVCAVLVTVGLSVARWLLGIOEGGCFRS--TRNFNSMRPPLL 178
DB 118 HPLRARELSRPROAAAVCAVVALWVTVSLVVRWLGWEGGCFSSQTRNFSTTAFSLL 177
QY 179 GFYLPVAVVFCSLKVVTALAOQPPDVGQAETRAKRMVWNLVVFVVCFLPHVGLT 238
DB 178 GFYLPVAVVFCSLQVTVLSRPAADVQAETQKATMVWNLAVFVICFLPHVGLT 237
QY 239 VRLAVGNACALLETIRRLYITSKLSDANCLDAICYYTMAKEFOEASALAVAPRAKAH 298
DB 238 VQVSLNLTCAARDTFSRLSITGKLSLSDTNCCLDAICYYTMAKEFOEAFKATSSNT-PH 296
QY 299 KSQDSLCVTL 308
DB 297 KSQYSQILSL 306
RESULT 10
Q4TAHO TETNG PRELIMINARY; PRT; 305 AA.
AC Q4TAHO;
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Chromosome 1 SCAF7335, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTENG00004207001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anhouart V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brotier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., Mesirov J.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

RA O'Dowd B.F., Nguyen T., Jung B.P., Marchese A., Cheng R., Heng H.H.Q.,
 RA Kolakowski L.F. Jr., Lynch K.R., George S.R.;
 RT "Cloning and chromosomal mapping of four putative novel human G-
 RT protein-coupled receptor genes.";
 RL Gene 187:75-81(1997).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RA Bohm S.K., Khatin L.M., Payan D.P., Bunnett N.W.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=9736605; PubMed=9223435; DOI=10.1006/bbrc.1997.6895;
 RA Janssens R., Boeynaems J.M., Godart M., Communi D.;
 RT "Cloning of a human heptahelical receptor closely related to the p2Y5
 RT receptor";
 RL Biochem. Biophys. Res. Commun. 236:106-112(1997).
 RN [4]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15772651; DOI=10.1038/nature03440;
 RA Ross M.T., Grafham D.V., Coffey A.J., Scherer S., McLay K., Muzny D.,
 RA Platzer M., Howell G.R., Burrows C., Bird C.P., Frankish A.,
 RA Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R., Wen G.,
 RA Jones M.C., Hultles M.E., Andrews T.D., Scott C.E., Searle S.,
 RA Ramser J., Whittaker A., Deadman R., Carter N.P., Hunt S.E., Chen R.,
 RA Cree A., Gunaratne P., Haylak P., Hodgson A., Metzker M.L.,
 RA Richards S., Scott G., Steffen P., Sodergren E., Wheeler D.A.,
 RA Worley K.C., Alnscough R., Ambrose K.D., Ansari-Lari M.A., Aradhya S.,
 RA Ashwell R.I., Babbage A.K., Bagguley C.P., Ballabio A., Banerjee R.,
 RA Barker G.E., Barlow K.P., Barrett I.P., Bates K.N., Beare D.M.,
 RA Brasley H., Beasley O., Beck A., Bethel G., Blechschmidt K., Brady N.,
 RA Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
 RA Bruford E.A., Buhay C., Burch P., Burford D., Burgess J., Burrill W.,
 RA Burton J., Bye J.M., Carder C., Carrel L., Chako J., Chapman J.C.,
 RA Chavez D., Chen G., Chen Y., Clarke G., Clee C.M., Clegg S.,
 RA Clerc-Blankenburg K., Clifford K., Cobley V., Cole C.G., Conquer J.S.,
 RA Corby N., Connor R.E., David R., Davies J., Davis C., Davis J.,
 RA Delgado O., Deshazo D., Dhani P., Ding Y., Dinh H., Dodsworth S.,
 RA Draper H., Dugan-Rocha S., Dunham A., Dunn M., Durbin K.J., Dutta I.,
 RA Eades T., Ellwood M., Emery-Cohen A., Errington H., Evans K.L.,
 RA Faulkner L., Francis F., Frankland J., Fraser A.E., Galgoczy P.,
 RA Gilbert J., Gill R., Gloeckner G., Gregory S.G., Gribble S.,
 RA Griffiths C., Grocock R., Gu Y., Gwilliam R., Hamilton C., Hart E.A.,
 RA Hawes A., Heath P.D., Heilmann K., Hennig S., Hernandez J.,
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 RA de Jong P.J., Joseph S.S., Keenan S., Kelly S., Karshaw J.K., Khan Z.,
 RA Kiosch P., Klages S., Knights A.J., Kosiura A., Kovar-Smith C.,
 RA Laird G.K., Langford C., Lawlor S., Leversha M., Lewis L., Liu W.,
 RA Lloyd C., Lloyd D.M., Loulseged H., Loveland J.E., Lovell J.D.,
 RA Lozado R., Lu J., Lyne R., Ma J., Maheshwari M., Matthews L.H.,
 RA McDowell J., McLaren S., McMurray A., Meidl P., Meitinger T.,
 RA Milne S., Miner G., Mistry S.L., Morgan M., Morris S., Mueller I.,
 RA Mullikin J.C., Nguyen N., Nordsiek G., Nyakatura G., O'dell C.N.,
 RA Okwuonu G., Palmer S., Pandian R., Parker D., Parrish J.,
 RA Pasternak S., Patel D., Pearce A.V., Pearson D.M., Pelan S.E.,
 RA Perez L., Porter K.M., Ramsey Y., Reichwald K., Rhodes S.,
 RA Ridler K.A., Schlesinger D., Schueler M.G., Shra H.K.,
 RA Shaw-Smith C., Shen H., Sheridan E.M., Shownkeen R., Skuce C.D.,
 RA Smith M.L., Sotharan E.C., Steingrubner H.E., Steward C.A., Storey R.,
 RA Swann R.M., Swarbreck D., Tabor P.E., Taudien S., Taylor T.,
 RA Teague B., Thomas K., Thorpe A., Timms K., Tracey A., Trevanion S.,
 RA Tromans A.C., d'Urso M., Verduzco D., Villaseana D., Waldron L.,
 RA Wall M., Wang Q., Warren J., Warry G.L., Wei X., West A.,
 RA Whitehead S.L., Whiteley M.N., Wilkinson J.E., Willey D.L.,
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RA Zorilla S., Buck D., Reinhardt R., Poustka A., Rosenthal A.,
 RA Lehrach H., Meindl A., Minx P.J., Hillier L.W., Willard H.F.,
 RA Wilson R.K., Waterston R.H., Rice C.M., Vaudin M., Coulson A.,
 RA Nelson D.L., Weinstein G., Sulston J.E., Durbin R., Hubbard T.,
 RA Gibbs R.A., Beck S., Rogers J., Bentley D.R.;
 RT "The DNA sequence of the human X chromosome.";
 RL Nature 434:325-337(2005).
 RN [6]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zerborg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitney M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Not detected in the brain regions thalamus,
 CC putamen, caudate, frontal cortex, pons, hypothalamus and
 CC hippocampus.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; U66578; AAC51301.1; -; Genomic DNA.
 CC EMBL; U90323; AAB62087.1; -; Genomic DNA.
 CC EMBL; U90322; AAB62088.1; -; mRNA.
 CC EMBL; AF005419; AAB66322.1; -; Genomic DNA.
 CC EMBL; AY301274; AAF58404.1; -; Genomic DNA.
 CC EMBL; AL590083; CAD18851.1; -; Genomic DNA.
 CC EMBL; BC074722; AAH74722.1; -; mRNA.
 CC PIR; JC5549; JCS5549.
 CC HSP; P34996; IDDD.
 CC Ensembl; ENSG00000147145; Homo sapiens.
 CC HGNC; HGNC:4478; GPR23.
 CC MM; 300086; -.
 CC GO; GO:0005887; C: integral to plasma membrane; TAS.
 CC GO; GO:0004930; P: G-protein coupled receptor activity; TAS.
 CC GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; TAS.
 CC InterPro; IPR00276; GPCR_Rhodopsn.
 CC InterPro; IPR002188; P2Y5_purinceptor.
 CC Pfam; PF00001; 7tm1.1; 1.
 CC PRINTS; PR00237; GPCR_Rhodopsn.
 CC PRINTS; PR01067; P2Y5ORPHAN.
 CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
 CC Transmembrane. 1 43 Extracellular (Potential).
 CC TOPO_DOM 44 64 1 (Potential).
 CC TRANSMEM 44 64 1 (Potential).
 CC TOPO_DOM 65 73 Cytoplasmic (Potential).
 CC TRANSMEM 74 94 2 (Potential).
 CC TOPO_DOM 95 112 Extracellular (Potential).
 CC TRANSMEM 113 133 3 (Potential).
 CC

GN Name=Gpr23;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akazawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Akizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Straubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tsgami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AK051709; BAC34729.1; -; mRNA.
DR MGI; MGI:1925384; Gpr23.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G- . . ; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR002188; GPCR Rhodopsin.
DR InterPro; IPR002188; P2Y5_purinceptor.
DR Pfam; PF00001; 7tm.1.1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PRINTS; PR01067; P2Y5ORPHAN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; UNKNOWN_1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR FL2; 1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 370 AA; 41956 MW; AB126842343AE6E1 CRC64;
Query Match 24.7%; Score 399; DB 2; Length 370;
Best Local Similarity 34.3%; Pred. No. 7.9e-22;
Matches 104; Conservative 59; Mismatches 112; Indels 28; Gaps 11;
QY 4 TYNTGSSDLTWPAPKLGYPAYLVGLVLLVGLLLSLVWVFCRCRQMQQTETRIYMTNL 62
DB 27 TNNTICVDD-----SFKNLNGAVYSVVFILGLITNSASLFFVFCRMRKSETAIFITNL 81
QY 63 AVADLCCLCTLPF-VLHSLR---DTSDTPLCQLSQGIYLTNRNYSISLVTAIAVDYXVAV 118
DB 82 ALSDLFLVCTLPFKIFYNFNHWPFGDT-LCKISGTAFNLINYSMLFLTCISVDRLAI 140
QY 119 RHPRLARGLRSPROAAVAVLVVIGSLVARMLLQIE-----GGFCFRSTRHN 169
DB 141 VYFPRSTIRTRNSAIVCAGVWILVNGGISLFTSTNNVNNATTTTCFEGSKRVWKTY 200
QY 170 FNSMR--FPILGLFVLPLAVVFCSLKVVTALAQRPPTDVQAEAT-RKAKEMVWNLVVF 226
DB 201 LSKITIFIEVVGFIPLILNVSCSVVLRTL--RKPATLSQIGTNKKKVLKMTVTHWAVF 258
QY 227 VVCFPLHVLGTVRLAVGNAC--ALLETRRRLY-ITSKLSDANCCLDACIYYMAKEF 283
DB 259 VVCFVPSNVLFYLYVRSQAITNCLERFAKINYPITLCLATLNCDFDPFIYFTLBSF 318
QY 284 QEA 286
DB 319 QKS 321
RESULT 15
Q8BLG2 MOUSE PRELIMINARY; PRT; 370 AA.
AC Q8BLG2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length
DE enriched library, clone: B130055L15 product: P2Y PURINOCEPTOR 9, full
DE insert sequence.
GN Name=Gpr23;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

RX NCBI_TaxID=10090;
 RN [1]_TaxID=10090;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Konno S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Pleischmann W., Gaasterland T., Giasi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RA The FANTOM Consortium.
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
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 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
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 sequencing pipeline with 384 multicapillary sequencer.";
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 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC 1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
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 DR Ensemble; ENSMUSG00000049929; Mus musculus.
 DR MGI; MGI:1925384; Gpr23.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G- . . ; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . ; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000276; GPCR Rhodopsn.
 DR InterPro; IPR002188; P2Y5_purinocptor.
 DR Pfam; PF00001; 7tm 1, 1.
 DR PRINTS; PRO0237; GPCRHOPOPSN.
 DR PRINTS; PRO1087; P2Y5ORPHAN.
 DR PROSITE; PS00237; G PROTEIN RECP_F1_1; UNKNOWN 1.
 DR PROSITE; PS0262; G PROTEIN RECP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 370 AA; 41872 MW; 084C79FEDFD32050 CRC64;
 Query Match 24.2%; Score 391; DB 2; Length 370;
 Best Local Similarity 34.5%; Pred. No. 3.1e-21;
 Matches 97; Conservative 59; Mismatches 103; Indels 22; Gaps 9;
 QY 25 AVIGLVLLVGLLNSLALWVFCRCMQQWETRIYMTNLAVADLCILCTLPV-VLHSLR-- 81
 DB 44 AVYSVVFILGLITSSASLVFVCFRMRKMSRTAIFITNLALSLLVFCVLTLPFFKIFYNRHH 103
 QY 82 -DTSDTPLCOLSQGIYLTNRYSISLVTAIAVDYVAVRHPLRARGLSRPRQAAAVCAVL 140
 DB 104 WFFGDT-LCKISGTAFNLINIGSMLFLACISVDRLAIVYPRSTRITRNSAIVCAGV 162
 QY 141 WVLVGTSLVARMLLQIE-----GGPCFRSTRHNFNSMR--PPLIGFYPLAVVVF 189
 DB 163 WILVLSGGGISASLFSSTTVNNATTTTCFEGSKRVKTYLSKITIFIEVVGFIPLILNVS 222
 QY 190 CSLKVVVTAALQRPPTDVGQAEAT-RKAKRMVWNLVVFVVCPLPLHVLGTVPLAVQWNA 248
 DB 223 CSVVVLRITL--RKPATLSQIGTNKKVKLVKMTVHMAVVFVCPVYNVSLFLYALVRSQAI 280
 QY 249 --ALLETRRALY-ITSKLSDANCCCLDAICYYYMAKEFOEA 286
 DB 281 TNCLLERPAKIMYPITLCIATLNCDFDPPIYYFTLESFQKS 321
 Search completed: February 9, 2006, 01:00:18
 Job time : 166.5 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 01:00:39 ; Search time 33.5 Seconds
(without alignments)
762.591 Million cell updates/sec

Title: US-10-083-168-85
Perfect score: 1615
Sequence: 1 MNGTYNTCGSSDLTWPPIAK.....AVAPRAKAHKSQDSLVCVTILA 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: Issued Patents AA:*
 - 2: /cgm2_6/ptodata/1/iaa/5 COMB.pep.*
 - 3: /cgm2_6/ptodata/1/iaa/6 COMB.pep.*
 - 4: /cgm2_6/ptodata/1/iaa/H-COMB.pep.*
 - 5: /cgm2_6/ptodata/1/iaa/RE-COMB.pep.*
 - 6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1609	99.6	309	2	US-09-422-869-20
2	401	24.8	370	2	US-08-781-250-2
3	382.5	23.7	363	2	US-10-314-048A-159
4	376.5	23.3	363	2	US-10-314-048A-36
5	374.5	23.2	387	2	US-09-170-496D-222
6	369.5	22.9	387	2	US-09-170-496D-108
7	369.5	22.9	387	2	US-09-944-807-21
8	369.5	22.9	387	2	US-10-314-048A-135
9	360.5	22.3	344	1	US-08-467-948A-8
10	360.5	22.3	344	2	US-08-467-947A-8
11	360	22.3	372	2	US-09-875-076-4
12	359.5	22.3	302	1	US-08-467-948A-30
13	359.5	22.3	302	2	US-08-467-947A-30
14	348.5	21.6	360	2	US-10-314-048A-137
15	340.5	21.1	351	2	US-10-314-048A-157
16	340	21.1	361	2	US-10-314-048A-139
17	329.5	20.4	254	2	US-09-964-956-83
18	328.5	20.3	377	2	US-09-745-842-17
19	327.5	20.3	374	2	US-09-102-710B-3
20	326	20.2	346	2	US-10-314-048A-24
21	323.5	20.0	346	2	US-10-314-048A-88
22	321.5	19.9	345	2	US-09-979-603-18
23	320	19.8	362	2	US-08-513-974B-374
24	319.5	19.8	343	2	US-10-314-048A-151
25	318.5	19.7	346	2	US-09-585-876-2
26	317.5	19.7	391	2	US-09-826-509-463
27	316.5	19.6	346	2	US-09-979-603-2

28	316.5	19.6	346	2	US-10-314-048A-14	Sequence 14, Appl
29	316	19.6	309	2	US-09-979-603-22	Sequence 22, Appl
30	316	19.6	374	2	US-09-745-842-15	Sequence 15, Appl
31	315.5	19.5	365	2	US-09-745-842-16	Sequence 16, Appl
32	315.5	19.5	365	2	US-09-077-173D-2	Sequence 2, Appli
33	315	19.5	373	2	US-08-513-974B-373	Sequence 373, App
34	311.5	19.3	354	2	US-09-364-425B-60	Sequence 60, Appl
35	311.5	19.3	362	2	US-09-170-496D-4	Sequence 4, Appli
36	311.5	19.3	362	2	US-09-850-948-2	Sequence 2, Appli
37	311.5	19.3	364	2	US-08-148-708-2	Sequence 2, Appli
38	310.5	19.2	358	2	US-09-170-496D-186	Sequence 186, App
39	310	19.2	342	2	US-09-826-509-555	Sequence 555, App
40	309	19.1	342	2	US-08-988-876-9	Sequence 9, Appli
41	307.5	19.0	362	2	US-09-170-496D-166	Sequence 166, App
42	306.5	19.0	375	1	US-08-442-134A-2	Sequence 2, Appli
43	306.5	19.0	375	1	US-08-444-581B-2	Sequence 2, Appli
44	306.5	19.0	375	1	US-08-446-088A-2	Sequence 2, Appli
45	306.5	19.0	375	1	US-08-559-524A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-422-869-20
; Sequence 20, Application US/09422869
; Patent No. 6235481
; GENERAL INFORMATION:
; APPLICANT: POLONSKI, KENNETH S.
; APPLICANT: HORIKAWA, YUKIO
; APPLICANT: ODA, NAOHISA
; APPLICANT: COX, NANCY J.
; APPLICANT: SEENAN, SEAMUS
; APPLICANT: ZHOU, YUN-PING
; APPLICANT: OTANI, KENICHI
; APPLICANT: HANIS, CRAIG L.
; APPLICANT: BELL, GRAEME I.
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
; FILE REFERENCE: ARCD:307
; CURRENT APPLICATION NUMBER: US/09/422,869
; CURRENT FILING DATE: 1999-10-21
; EARLIER APPLICATION NUMBER: 60/134,175
; EARLIER FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Human
US-09-422-869-20

Query Match	99.6%;	Score 1609;	DB 2;	Length 309;
Best Local Similarity	99.7%;	Pred. No. 8.1e-133;		
Matches 308;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLNSLALWVFCRMOQTETRIYMT	60	
Db	1	MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVLGLLNSLALWVFCRMOQTETRIYMT	60	
Qy	61	NLAVALDLCLCTLPFVLHSLRDTSDTLPCLQSQSGLYLTNRYSISLVTAIADRYAVRH	120	
Db	61	NLAVALDLCLCTLPFVLHSLRDTSDTLPCLQSQSGLYLTNRYSISLVTAIADRYAVRH	120	
Qy	121	PLRARGLRSPQAAAVCAVLWLVIGSLVAVLWLIQEGGCFRSTRNFMSPPLLGF	180	
Db	121	PLRARGLRSPQAAAVCAVLWLVIGSLVAVLWLIQEGGCFRSTRNFMSPPLLGF	180	
Qy	181	YLPLAVVFCSLKVVTALAQRPPTDVGQAEATRAKRWANLLVVFVVCFLPLHVLTVR	240	
Db	181	YLPLAVVFCSLKVVTALAQRPPTDVGQAEATRAKRWANLLVVFVVCFLPLHVLTVR	240	
Qy	241	LAVGWNCALLETIRRALYITSKLSDANCCDLDAICYYTMAKEFOEASALAVAPRAKHS	300	

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Db      241  LAVGMNACALLETIRRALYITTSKLSDANCCLDAICYYTMAKFBQEKASALAVAPRAKAHKS 300

Qy      301  QDSLCLVTLA 309
        |||||
Db      301  QDSLCLVTLA 309

RESULT 2
US-08-781-250-2
; Sequence 2, Application US/08781250
; Patent No. 6010877
; GENERAL INFORMATION:
;   APPLICANT: Sathe, Ganesh
;   APPLICANT: Van Horn, Stephanie
;   APPLICANT: Bergsma, Derk
;   APPLICANT: Mao, Joyce Yue
;   TITLE OF INVENTION: CDNA CLONE H8CS41 THAT ENCODES A NOVEL 7-TRANSMEMBRAN
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Smithkline Beecham
;     STREET: 709 Swedeland Road
;     CITY: King of Prussia
;     STATE: PA
;     COUNTRY: USA
;     ZIP: 19406
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSeq for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/781,250
;     FILING DATE: 10-JAN-1997
;     CLASSIFICATION: 514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME: William T. Han,
;       REGISTRATION NUMBER: 34,344
;       REFERENCE/DOCKET NUMBER: ATGS0043
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 610-270-5219
;       TELEFAX: 610-270-4060
;     TELEX:
;   INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 370 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
;   US-08-781-250-2;

Query Match      24.8%; Score 401; DB 2; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.8e-27;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

Qy      25  AYGVLIVLGLLNSIALWVFCCRMQOWTETRIYMTNLAVADCLLCTLPF-VLHSLR-- 81
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      44  AVYSVVFIQLITNSVSLFVFCPRMQRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

Qy      82  -DTSDFPLCQLSGIYLTNRYMSISLVTAIADRYVAVPHPLRAGLSPRQAAACAVL 140
        || : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      104  WPGEDT-LCKISGTAFLTNIYGSMLPLTCSIVDRFLAIVYPRSRITIRRNSAIVCAGV 162

Qy      141  WVLVIGSLVARNMLLIGQE-----GGFCFRSTRNFNFSMR--FPLIGFYLPVAVVVF 189
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      163  MILVLSGGSISLFSITNNVNAITTCFEGFSKRVKYLISKITIEVVGFIPLILNVS 222

Qy      190  CSLKVTVALAQRPTDVQGAET-RKAKRMVWANLLVFWVCFPLPHVGLTVRLAVGNAC 248
        || : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      223  CSBVLRLT--RKPAFLSGIGTNKKKVLKMTTHMAVFVYCFVFNYSVLFLYALVRSQAI 280

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Db 264 QNCEVRSVDLAFFITLSFTYNSMLDPVYVYFSSPSF 301

RESULT 4

US-10-314-048A-36
; Sequence 36, Application US/10314048A

; Patent No. 6902902

; GENERAL INFORMATION:

; APPLICANT: Unett, David J.

; APPLICANT: Chen, Ruoping

; APPLICANT: Richman, Jeremy

; APPLICANT: Connolly, Daniel

; APPLICANT: Dang, Huong T.

; APPLICANT: Choi, Bryan

; APPLICANT: Leonard, James

; APPLICANT: Hakak, Yaron

; APPLICANT: Liaw, Chen

; APPLICANT: Lowitz, Kevin P.

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Lerner, Michael

; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof

; FILE REFERENCE: 22 US6.CIP

; CURRENT APPLICATION NUMBER: US/10/314,048A

; CURRENT FILING DATE: 2002-12-06

; PRIOR APPLICATION NUMBER: 10/096,511

; PRIOR FILING DATE: 2002-03-12

; PRIOR APPLICATION NUMBER: 09/995,543

; PRIOR FILING DATE: 2001-11-27

; PRIOR APPLICATION NUMBER: 60/399,917

; PRIOR FILING DATE: 2002-07-29

; PRIOR APPLICATION NUMBER: 60/404,761

; PRIOR FILING DATE: 2002-08-19

; PRIOR APPLICATION NUMBER: 60/410,747

; PRIOR FILING DATE: 2002-09-13

; NUMBER OF SEQ ID NOS: 161

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 36

; LENGTH: 363

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-314-048A-36

Query Match 23.3%; Score 376.5; DB 2; Length 363;

Best Local Similarity 34.8%; Pred. No. 6.3e-25;

Matches 97; Conservative 45; Mismatches 104; Indels 33; Gaps 11;

Qy 27 LGVLLVGLLNSLALWVFCRCMQWTETRIYMTNLAVADCLLCTLPFVLHSL-----R 81

Db 34 LGLEFIFGLLNGLALWIFCFHLKSWKSSRIFLNFNLAVADFLIICLPFLMDNVYRRWDW 93

Qy 82 DTSPTPLCQLSQGIYLTNRNYSISLVTAIAVDYVAVRHPLRARGLRSPROAAAVCAVLW 141

Db 94 KFGDIP-CLMLFPLMNRQCSIIFLTVAVDYVAVRHPLRARGLRSPROAAAVCAVLW 152

Qy 142 VLVIGSLV--ARWLGIGEGG--FCFR-STRHNF--NSMRPPLGFLYPLAVVVFVCSLKV 194

Db 153 GITIGLTVHLKKKKPIQNGGANLCSFSICHTFQWHEAMF-LLEFFLPLGLIILFCSARI 211

Qy 195 VTALAQRPTDVGQAEATRKAKR-----MYWANLLVTVVCFPLPHVGLTVRLAVGW----- 245

Db 212 IWSLQR-----QMDRHAKIKRAITFMVVAIVFVICFLP---SVVVRIRIFMLLHTSG 262

Qy 246 -NACALLTETIRRALYITSKLSDANCLDAICYVYMAKEF 283

Db 263 TQNCVRSVDLAFFITLSFTYNSMLDPVYVYFSSPSF 301

RESULT 5

US-09-170-496D-222

; Sequence 222, Application US/09170496D

; Patent No. 6555339

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: AREN-0040

; CURRENT APPLICATION NUMBER: US/09/170,496D

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 294

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 222

; LENGTH: 387

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-170-496D-222

Query Match 23.2%; Score 374.5; DB 2; Length 387;

Best Local Similarity 34.4%; Pred. No. 1e-24;

Matches 95; Conservative 47; Mismatches 107; Indels 27; Gaps 10;

Qy 27 LGVLLVGLLNSLALWVFCRCMQWTETRIYMTNLAVADCLLCTLPFVLHSLRDTSDT 86

Db 34 LGLEFIFGLLNGLALWIFCFHLKSWKSSRIFLNFNLAVADFLIICLPFVMDYVYRRSDW 93

Qy 87 PL-----COLSQGIYLTNRNYSISLVTAIAVDYVAVRHPLRARGLRSPROAAAVCAVLW 142

Db 94 KFGDIP-CLRLVLFPMNRQCSIIFLTVAVDYVAVRHPLRARGLRSPROAAAVCAVLW 153

Qy 143 LVIG-----SLVARMLGIGEG--GFCFR-STRHNF--NSMRPPLGFLYPLAVVVFVCSLKV 194

Db 154 ITVGLTVHLKKKLL-IQNGPANVCISFSICHTFRWHEAMF-LLEFFLPLGLIILFCSARI 211

Qy 195 VTALAQRPTDVGQAEATRKAKRMYWANLLVTVVCFPLPHVGLTVRLAVGW-----NA 247

Db 212 IWSLQR-----QMDRHAKIKRAITFMVVAIVFVICFLP---SVVVRIRIFMLLHTSGTON 265

Qy 248 CALLETIRRALYITSKLSDANCLDAICYVYMAKEF 283

Db 266 CEVRSVDLAFFITLSFTYNSMLDPVYVYFSSPSF 301

RESULT 6

US-09-170-496D-108

; Sequence 108, Application US/09170496D

; Patent No. 6555339

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: AREN-0040

; CURRENT APPLICATION NUMBER: US/09/170,496D

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 294

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 108

; LENGTH: 387

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-170-496D-108

Query Match 22.9%; Score 369.5; DB 2; Length 387;

Best Local Similarity 35.0%; Pred. No. 2.7e-24;

Matches 98; Conservative 45; Mismatches 102; Indels 35; Gaps 12;

Qy 27 LGVLLVGLLNSLALWVFCRCMQWTETRIYMTNLAVADCLLCTLPFVL-----HSILR 81

Db 34 LGLEFIFGLLNGLALWIFCFHLKSWKSSRIFLNFNLAVADFLIICLPFVMDYVYRRSDW 93

Qy 82 DTSPTPLCQLSQGIYLTNRNYSISLVTAIAVDYVAVRHPLRARGLRSPROAAAVCAVLW 141

CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-948A-8

Query Match	22.3%	Score	360.5	DB 1	Length	344			
Best local Similarity	29.2%	Pred. No.	1.4e-23						
Matches	90	Conservative	68	Mismatches	107	Indels	43	Gaps	10

Qy	10	SSDLTPPAIKGFAVYLGVLLVLGLLLNSLALWVFCRQMOWTEIRYVMTNLAVADLC	68
Db	6	SSHCFYNDSPKTYLGYCMFSWVFLVGLLISNCVAIYIFCVLKVNRNITTYMINLAMSDLL	65
Qy	69	LLCTLPVFLSHSLRDTSDTP-----LCQLSQGIYLTNRNYSISLVTAIAVDRVAVVRHPLRA	124
Db	66	FVFTLPFRIFYF--TTRNWPFGDLLCKISVWMLFYTNMYGSLFLTCLISVDRFLAIVYPPKS	124
Qy	125	RGLRSPQAAAVCAVLVVLVI--GSLVARWLLGIOBGG-----FCERSTRHFNPSMRPP--	176
Db	125	KTLRTKRNAKIVCTGVMLTVIGGSAPAFVQSTHSQGNNASEACFEN-----PPEA	175
Qy	177	-----LLGFPVLPAVVVFCSLKVVTALAQRPPTDVGQAEATR--KAKRMVWA	221
Db	176	TWKTYLSRIVTIFRIVGPFPLILNVTCSWVWKLTKLR--PVTLSRSKINKTKVLKMLFV	233
Qy	222	NLLVFWVCFLPLHVGLTVRLAVGWNA---CALLETIRREALYITSKLSDANCLDAICYYY	278
Db	234	HLIIFCFCFVYPYNILYSLVRTQTFVNCVSVAARWTMYPITLCLAVSNCCFDIVVYF	293
Qy	279	MAKEFQEA	286
Db	294	TSDTIONS	301

RESULT 10
US-08-467-947A-8
; Sequence 8, Application US/08467947A
; Patent No. 6090575
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BULT, CAROL J.
; APPLICANT: SUTTON III, GRANGER G
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Polynucleoti

TITLE OF INVENTION: Coupled Receptor GPR1
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,947A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04079
 FILING DATE: 30-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: STEFFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 344 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-467-947A-8

Query Match	22.3%	Score	360.5	DB 2	Length	344			
Best Local Similarity	29.2%	Pred. No.	1.4e-23						
Matches	90	Conservative	68	Mismatches	107	Indels	43	Gaps	10
Qy	10	SSDLTWPPA	AIKLGFAVYL	GVLLVLGLLLNSLALWVFCRMRQOWTETRIYMTNLAVADLC	68				
Db	6	SSHCFYND	SFKYTYGCMF	SMVFLVGLISNCVAIYIFCVLKVRNETTYMINLAMSDLL	65				
Qy	69	LLCTLFPVLH	SLRDTSDTP	----LCQLSQGIYLTNRNYSISLVAITAIVDRVAVVRHPLRA	124				
Db	66	FVETLPR	IFRIFYF	-TTRNPFQDGLCKISVMLFYTNMYGSIILFLTCISVDRLAIVYPEKS	124				
Qy	125	RGLRS	PROAAVCAVL	VLVI-GSLVARWLLGIOEGG-----FCFSTRHFNFSNRFP--	176				
Db	125	KTLTRK	NAKIVCTGVMLTV	IGSSAPAFVQSTHSGQNNASEACFEN-----FPFA	175				
Qy	177	-----LLG	PYLP	PLAVVFCSLKVVATAAQRPTDVGQAETR-KAKRMVWA	221				
Db	176	TKWTVLSR	IVIFIEIVG	FFELIINLVTCSSWVLTLYK--PVTLSRSKINKTKVLKMLFV	233				
Qy	222	NLLVFWVC	FPLPLRVGLT	VRLVAGWNA---CALLERTREALYITSKLSANDCCLDAICYY	278				
Db	234	HLIIFC	FCFVFNINIL	YSLVTRQTFVNCVSVVAARWTYPIITLCIAVSNCCFDPIVYVY	293				
Qy	279	MAKBFQEA		286					
Db	294	TSDTIONS		301					

RESULT 11
US-09-875-076-4
; Sequence 4, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chong W.

APPLICANT: Lin, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors

FILE REFERENCE: AREN0050

CURRENT APPLICATION NUMBER: US/09/875,076

CURRENT FILING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: 09/417,044

PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: 60/120,416

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: 60/121,851

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/123,946

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,949

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/136,436

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,437

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,439

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/136,567

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/137,127

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/137,131

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/141,448

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: 60/156,653

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/156,633

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/156,555

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/156,634

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: 60/157,280

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/157,294

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/157,281

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/157,293

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 60/157,282

PRIOR FILING DATE: 1999-10-01

NUMBER OF SEQ ID NOS: 74

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 4

LENGTH: 372

TYPE: PRT

ORGANISM: Homo sapiens

US-09-875-076-4

Query Match 22.3%; Score 360; DB 2; Length 372;

Best Local Similarity 33.7%; Pred. No. 1.7e-23;

Matches 109; Conservative 47; Mismatches 125; Indels 42; Gaps 12;

QY 6 NTGSGDLTWP---PAIKGFYAYLGVLVGLLNSLALWVFCRMOQWETRIYMTNL 62

Db 6 SSTNSVLPCPDYRPHRTLHLVY-SLVLAAGLPLNALWVFLRLRVHVSVMCMNL 64

QY 63 AVADLCCLCTLP-----FVLHSLRSDTDP-----LCQLSQGIYLTNRYSISLVTAIYD 113

Db 65 RASDLLPTLSLPLVRLSYALH-----HWFPDLCQTTGAIFQNMVYSCIFLMLIND 118

QY 114 RVAVRHPLRAGLRSPQAAVCAVLWVLVIGSLV-----ARWLIGIOEGGCFPS 165

Db 119 RYAAIVHPLRLHRLRRPRVARLLCLGVWALILVFAVPAARVHRPSRCRYRDLVRLCFPS 178

QY 166 -TEHFNNSRFP-----LGFVLPLAVVFCSLKVVLTALQRPPTDVGQAETRAKEM 218

Db 179 FSDLMKGRLLPLVLLAEALGFLPLAAVVYSSGRVFWTLA-RP--DATSQRRRTVRL 235

QY 219 VMANLVFVVCFLPLHVLTV----RLAVGWACALLETIRRALYITSKLSANDCLDAI 274

Db 236 LLANLVIFLLCFVYNSTLAVYGLLRSLKVAASVPARDVRGVLMVMVLLAGANCVDPL 295

QY 275 CYYMAKEFOEA-SALAVAPRAK 296

Db 296 VYFSAEGFRNTLRGLGTPHRAK 318

RESULT 12

US-08-467-948A-30

Sequence 30, Application US/08467948A

Patent No. 5998164

GENERAL INFORMATION:

APPLICANT: LI, YI

APPLICANT: CAO, LIANG

APPLICANT: NI, JIAN

APPLICANT: GENTZ, REINER

APPLICANT: BULT, CAROL J.

APPLICANT: SUTTON III, GRANGER G.

APPLICANT: ROSEN, CRAIG A.

TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein

TITLE OF INVENTION: Coupled Receptor GPR2

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,948A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04079

FILING DATE: 30-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 302 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

US-08-467-948A-30

Query Match 22.3%; Score 359.5; DB 1; Length 302;

Best Local Similarity 30.0%; Pred. No. 1.5e-23;

Matches 90; Conservative 64; Mismatches 103; Indels 43; Gaps 10;

QY 10 SSDLTWPPAIKGFY-AYLGVLVGLLNSLALWVFCRMOQWETRIYMTNLAVADLC 68

Db 1 SSNCSTEDSFKTYLGCVFMSVFLGLIANCVAIYFTFLKVRNETTTTMLMLAISDLL 60

QY 69 LCLTLPFVLHSLRSDTDP-----LCQLSQGIYLTNRYSISLVTAIYDVRVYVVRHPLRA 124

Db 61 FVFTLFPRIIYP-VVRNWFPGDVLCKISVTLFYTNMYSILFCLTCLISVDRFLAIVHPPRS 119

Db 210 WSLRQ-----QMDRHAKIKRAINFIMVVAIVFIICFLP---SVAVRIRFWLLKYKNV 260
QY 246 NACALLETRRALYITSKLSDANCCLDACIYYMAKEP 283
Db 261 RNCDIYSSVDLAFFTLTSTYNNMMLDPVVYFSSPSF 298

RESULT 15

US-10-314-048A-157
; Sequence 157, Application US/10314048A
; Patent No. 6902902
; GENERAL INFORMATION:
; APPLICANT: Unett, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Huong T.
; APPLICANT: Choi, Bryan
; APPLICANT: Leonard, James
; APPLICANT: Hakak, Yaron
; APPLICANT: Liaw, Chen
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lerner, Michael
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; FILE REFERENCE: 22.US6.CIP
; CURRENT APPLICATION NUMBER: US/10/314,048A
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096,511
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/995,543
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/399,917
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/404,761
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/410,747
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 157
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Rat
US-10-314-048A-157

Query Match 21.1%; Score 340.5; DB 2; Length 351;
Best Local Similarity 33.2%; Pred. No. 8e-22;
Matches 107; Conservative 48; Mismatches 114; Indels 53; Gaps 15;
QY 16 PPAIKLGFYVLGVLLVGLLNSLALWVFCRCMQWQWETRIYMTNLAVADLCCLTLPF 75
Db 27 PELLILAF-----LLGALGNGLALCGCFHMTWKSTIYFLNLAVALDFLLMICPL 78
QY 76 -VLHSLRD---TSDFPLCQLSQGIYLTNRYSISLVTAIVDRYVAVRHPLEARGLRSP 130
Db 79 RTDYLLRRRHWILGDIIP-CRLVLFMLAMNRAGSIVFLTVVAVDRYFKVHPHMYNAISN 137
QY 131 ROAAAVCAVLWVLVIGSLVARMVLGIQEGGCFR-----STRNFNSMRPPLLG 179
Db 138 RTAAATVCVLTVILGTV--YLL--MESHLCVRGMVSSCSFIMESANGWHDIMFQ-LE 192
QY 180 FYLPLAVVVFCSLKVVYALAQRPPTDVQABATRAKRMVMANLLVYVVCPLPLHVLTV 239
Db 193 FFLPLTILFCFKVWVSLRQ--QQLTRQARMRATRFIMVVASVFITCILP----SVLA 247
QY 240 RLAVGW---NACALLETRRALYITSKLSDANCCLDACIYYMAKEPQEAASA----LAV 291
Db 248 RLYFLWTVFSSACD--PSVHIALHVTLSLYLNSMLDPLVYFSSPSPPKFKLIRSL 305

QY 292 AP-----RAKAHKSOD-----SLC 305
Db 306 KPRRPGRSQARRSEMPISNLC 327
Search completed: February 9, 2006, 01:02:28
Job time : 34.5 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 01:16:44 ; Search time 118.5 Seconds

(without alignments)
1089.530 Million cell updates/sec

Title: US-10-083-168-85

Perfect score: 1615

Sequence: 1 MNGTYTCGSSDLTWPPAIK.....AVAPRAKHKQDSLCVTLA 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgm2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1609	99.6	309	3	US-09-768-877-20
2	1609	99.6	309	4	US-10-225-567A-492
3	1609	99.6	309	5	US-10-696-639-44
4	1603	99.3	547	5	US-10-505-486-84
5	1597	98.9	309	4	US-10-157-031-351
6	401	24.8	370	3	US-09-964-821B-11
7	401	24.8	370	4	US-10-081-810-44
8	401	24.8	370	4	US-10-225-567A-225
9	401	24.8	370	4	US-10-024-298A-176
10	401	24.8	370	4	US-10-042-211A-176
11	401	24.8	370	4	US-10-268-332-11
12	401	24.8	370	4	US-10-617-217A-176
13	401	24.8	370	4	US-10-775-965-11
14	401	24.8	370	4	US-10-024-298A-176
15	401	24.8	370	5	US-10-753-267-86
16	401	24.8	608	5	US-10-505-486-114
17	400	24.8	370	3	US-09-964-821B-10
18	400	24.8	370	4	US-10-268-332-10
19	391	24.2	370	4	US-10-024-298A-174
20	391	24.2	370	4	US-10-042-211A-174
21	391	24.2	370	4	US-10-617-217A-174
22	391	24.2	370	4	US-10-024-298A-174
23	389	24.1	368	4	US-10-775-965-10
24	382.5	23.7	363	4	US-10-314-048A-159
25	382.5	23.7	363	5	US-10-897-815-159
26	382.5	23.7	363	5	US-10-930-662-159
27	377.5	23.4	363	3	US-09-930-334-16

ALIGNMENTS

RESULT 1

US-09-768-877-20

; Sequence 20, Application US/09768877

; Patent No. US20020150896A1

; GENERAL INFORMATION:

; APPLICANT: POLONSKI, KENNETH S.

; APPLICANT: HORIKAWA, YUKIO

; APPLICANT: ODA, NAOHISA

; APPLICANT: COX, NANCY J.

; APPLICANT: SREENAN, SEAMUS

; APPLICANT: ZHOU, YUN-PING

; APPLICANT: OTANI, KENICHI

; APPLICANT: HANIS, CRAIG I.

; APPLICANT: BELL, GRAEME I.

; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES

; FILE REFERENCE: ARCD:307

; CURRENT APPLICATION NUMBER: US/09768,877

; CURRENT FILING DATE: 2001-01-23

; PRIOR APPLICATION NUMBER: 09/422,869

; PRIOR FILING DATE: 1999-10-21

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 309

; TYPE: PRT

; ORGANISM: Human

US-09-768-877-20

Query Match 99.6%; Score 1609; DB 3; Length 309;

Best Local Similarity 99.7%; Pred. No. 6.9e-147; Indels 0; Gaps 0;

Matches 308; Conservative 0; Mismatches 1;

Qy	1	MNGTYTCGSSDLTWPPAIKLGFGYAYLGLVLGLLNSLALWVFCRQQTETRIYMT	60
Db	1	MNGTYTCGSSDLTWPPAIKLGFGYAYLGLVLGLLNSLALWVFCRQQTETRIYMT	60
Qy	61	NLAVALDCLLCTLPFVLHSLRSDTDPICQLSQGIYLTNRVMSISLVTIAVDRTVAVRH	120
Db	61	NLAVALDCLLCTLPFVLHSLRSDTDPICQLSQGIYLTNRVMSISLVTIAVDRTVAVRH	120
Qy	121	PIRAGLRSPQAAAVCAVLWLVIGSLVARWLLGIQGGCFRSTRNENSMRPLLCF	180
Db	121	PIRAGLRSPQAAAVCAVLWLVIGSLVARWLLGIQGGCFRSTRNENSMRPLLCF	180
Qy	181	YLPAAVVFCSLKVVTTALAQRPTDVQAEATRAKRWVWNLVVFVCFPLPHVGLTVR	240
Db	181	YLPAAVVFCSLKVVTTALAQRPTDVQAEATRAKRWVWNLVVFVCFPLPHVGLTVR	240
Qy	241	LAVGNACALLETTRRALYITTSKLSDNCCCLDAICYVYMAKEFOBASALAVAPRAKHS	300

Db 241 LAVGMNACALLETIRRALVITTSKLSDANCCLDAICYYYMAKEFQBSALAVAPRAKAHS 300

Qy 301 QBSLCVTLA 309
|||||

Dd 301 QBSLCVTLA 309

RESULT 2

US-10-225-567A-492
; Sequence 492, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn A.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 492
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-492

RESULT 4

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RES-011-4
US-10-505-486-84
; Sequence 84, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Determination of a ligand
; FILE REFERENCE: P03-0006PCT
; CURRENT APPLICATION NUMBER: US/10/505,486
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: JP 2002-298237
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 84
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Human
US-10-505-486-84

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RESULT 3

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RESUL1 3
US-10-696-639-44
/ Sequence 44, Application US/10696639
/ Publication No. US20050037439A1
/ GENERAL INFORMATION:
/ APPLICANT: Pharmacia Corporation
/ APPLICANT: Bourner, Maureen J.
/ TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
/ TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
/ FILE REFERENCE: 01040/1
/ CURRENT APPLICATION NUMBER: US/10/696,639
/ CURRENT FILING DATE: 2003-10-29
/ PRIOR APPLICATION NUMBER: 60/422,176
/ PRIOR FILING DATE: 2002-10-29

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/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: Patent in version 3.0
/ SEQ ID NO 44
/ LENGTH: 370
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-081-810-44

Query Match      24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AVLGVLVLGLLNSLALWFCRCMQWTEITRYMTNLAVADLCCLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVLSVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYFNHRH 103

QY 82 -DTSDFPLCOLSQGIYLTNRYSISLVTAIVADRYVAVRHPLRARGLRSPROAAACAVL 140
DB 104 WPGDGT-LCKISGTAFLTNIYGSMLFLTCISVDRFLAIYVPPFRSRTIRTRNSAIVCAGV 162

QY 141 WLVIGSLVARMLLGIQE-----GGFCFRSTRHNFSMR--PPLIGFYPLAVVVVF 189
DB 163 WILVLSGGISASLFTSTNNVNNATTCFEGFSKRVKTYLSKITPIFIEVVGFIPLINVS 222

QY 190 CSLKVVTALAQRPTDVGQAEAT--RKAKRMVWVANLLVFFVVCFLPLHVGTLVRLAVGWNAC 248
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVKLVKMITVHMAVFFVFCFVYNSVFLFLVALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCLDALCYIYMAKEFOEASALAVAPRAKAHKSQDSL 305
DB 281 TNCFLERPAKIMYPITLCLATLNCCDFPIIYFTLESFQKSFYI-----NAHIRMESLF 334

QY 306 VT 307
DB 335 KT 336

RESULT 8
US-10-225-567A-225
/ Sequence 225, Application US/10225567A
/ Publication No. US20030113798A1
/ GENERAL INFORMATION:
/ APPLICANT: LifeSpan Biosciences
/ APPLICANT: Brown, Joseph P.
/ APPLICANT: Roush, Christine L.
/ TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
/ FILE REFERENCE: 1920-4-4
/ CURRENT APPLICATION NUMBER: US/10/225,567A
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR FILING DATE: 2000-12-19
/ NUMBER OF SEQ ID NOS: 2292
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 225
/ LENGTH: 370
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-225-567A-225

Query Match      24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AVLGVLVLGLLNSLALWFCRCMQWTEITRYMTNLAVADLCCLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVLSVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYFNHRH 103

QY 82 -DTSDFPLCOLSQGIYLTNRYSISLVTAIVADRYVAVRHPLRARGLRSPROAAACAVL 140
DB 104 WPGDGT-LCKISGTAFLTNIYGSMLFLTCISVDRFLAIYVPPFRSRTIRTRNSAIVCAGV 162

QY 141 WLVIGSLVARMLLGIQE-----GGFCFRSTRHNFSMR--PPLIGFYPLAVVVVF 189
DB 163 WILVLSGGISASLFTSTNNVNNATTCFEGFSKRVKTYLSKITPIFIEVVGFIPLINVS 222

QY 190 CSLKVVTALAQRPTDVGQAEAT--RKAKRMVWVANLLVFFVVCFLPLHVGTLVRLAVGWNAC 248
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVKLVKMITVHMAVFFVFCFVYNSVFLFLVALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCLDALCYIYMAKEFOEASALAVAPRAKAHKSQDSL 305
DB 281 TNCFLERPAKIMYPITLCLATLNCCDFPIIYFTLESFQKSFYI-----NAHIRMESLF 334
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/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: Patent in version 3.0
/ SEQ ID NO 44
/ LENGTH: 370
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-081-810-44

Query Match      24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AVLGVLVLGLLNSLALWFCRCMQWTEITRYMTNLAVADLCCLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVLSVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYFNHRH 103

QY 82 -DTSDFPLCOLSQGIYLTNRYSISLVTAIVADRYVAVRHPLRARGLRSPROAAACAVL 140
DB 104 WPGDGT-LCKISGTAFLTNIYGSMLFLTCISVDRFLAIYVPPFRSRTIRTRNSAIVCAGV 162

QY 141 WLVIGSLVARMLLGIQE-----GGFCFRSTRHNFSMR--PPLIGFYPLAVVVVF 189
DB 163 WILVLSGGISASLFTSTNNVNNATTCFEGFSKRVKTYLSKITPIFIEVVGFIPLINVS 222

QY 190 CSLKVVTALAQRPTDVGQAEAT--RKAKRMVWVANLLVFFVVCFLPLHVGTLVRLAVGWNAC 248
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVKLVKMITVHMAVFFVFCFVYNSVFLFLVALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCLDALCYIYMAKEFOEASALAVAPRAKAHKSQDSL 305
DB 281 TNCFLERPAKIMYPITLCLATLNCCDFPIIYFTLESFQKSFYI-----NAHIRMESLF 334

QY 306 VT 307
DB 335 KT 336

RESULT 9
US-10-024-298A-176
/ Sequence 176, Application US/10024298A
/ Publication No. US20030143540A1
/ GENERAL INFORMATION:
/ APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
/ APPLICANT: AKIO MATSUDA
/ APPLICANT: Goichi HONDA
/ APPLICANT: Shuji MURAMATSU
/ APPLICANT: Yukiko NAGANO
/ TITLE OF INVENTION: NF-K B Activating Gene
/ FILE REFERENCE: 1254-0191P
/ CURRENT APPLICATION NUMBER: US/10/024,298A
/ CURRENT FILING DATE: 2003-04-08
/ PRIOR APPLICATION NUMBER: 60/314,385
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: 60/278,641
/ PRIOR FILING DATE: 2001-03-26
/ PRIOR APPLICATION NUMBER: 60/258,315
/ PRIOR FILING DATE: 2000-12-28
/ PRIOR APPLICATION NUMBER: JP254018/2001
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: JP008912/2001
/ PRIOR FILING DATE: 2001-03-26
/ PRIOR APPLICATION NUMBER: JP402288/2000
/ PRIOR FILING DATE: 2000-12-28
/ NUMBER OF SEQ ID NOS: 182
/ SOFTWARE: Patent in Ver. 2.0
/ SEQ ID NO 176
/ LENGTH: 370
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-024-298A-176

Query Match      24.8%; Score 401; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.1e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AVLGVLVLGLLNSLALWFCRCMQWTEITRYMTNLAVADLCCLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVLSVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYFNHRH 103

QY 82 -DTSDFPLCOLSQGIYLTNRYSISLVTAIVADRYVAVRHPLRARGLRSPROAAACAVL 140
DB 104 WPGDGT-LCKISGTAFLTNIYGSMLFLTCISVDRFLAIYVPPFRSRTIRTRNSAIVCAGV 162

QY 141 WLVIGSLVARMLLGIQE-----GGFCFRSTRHNFSMR--PPLIGFYPLAVVVVF 189
DB 163 WILVLSGGISASLFTSTNNVNNATTCFEGFSKRVKTYLSKITPIFIEVVGFIPLINVS 222

QY 190 CSLKVVTALAQRPTDVGQAEAT--RKAKRMVWVANLLVFFVVCFLPLHVGTLVRLAVGWNAC 248
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVKLVKMITVHMAVFFVFCFVYNSVFLFLVALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCLDALCYIYMAKEFOEASALAVAPRAKAHKSQDSL 305
DB 281 TNCFLERPAKIMYPITLCLATLNCCDFPIIYFTLESFQKSFYI-----NAHIRMESLF 334
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[illegible]

Db 335 KT 336

RESULT 15

US-10-753-267-86

Sequence 86, Application US/10753267

Publication No. US20050037946A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Steglano, Nancy E.

APPLICANT: Healy, Aileen

APPLICANT: Acton, Susan L.

APPLICANT: Galvin, Katherine M.

APPLICANT: Donoghue, Mary A.

APPLICANT: Rodriguez-Way, Amelie

APPLICANT: Tomlinson, James E.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,

TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,

TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,

TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,

TITLE OF INVENTION: 9380, 2569654, 33556, 44143, 32612, 10671, 261,

TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,

TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,

TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419

FILE REFERENCE: MPI03-003P1RNMNIM

CURRENT APPLICATION NUMBER: US/10/753,267

CURRENT FILING DATE: 2004-01-08

PRIOR APPLICATION NUMBER: US 60/439,683

PRIOR FILING DATE: 2003-01-13

PRIOR APPLICATION NUMBER: US 60/445,216

PRIOR FILING DATE: 2003-02-05

PRIOR APPLICATION NUMBER: US 60/448,036

PRIOR FILING DATE: 2003-02-18

PRIOR APPLICATION NUMBER: US 60/454,189

PRIOR FILING DATE: 2003-03-12

PRIOR APPLICATION NUMBER: US 60/457,541

PRIOR FILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: US 60/466,411

PRIOR FILING DATE: 2003-04-29

PRIOR APPLICATION NUMBER: US 60/469,041

PRIOR FILING DATE: 2003-05-08

PRIOR APPLICATION NUMBER: US 60/477,414

PRIOR FILING DATE: 2003-06-10

PRIOR APPLICATION NUMBER: US 60/478,560

PRIOR FILING DATE: 2003-06-13

PRIOR APPLICATION NUMBER: US 60/489,772

PRIOR FILING DATE: 2003-07-24

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 130

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 86

LENGTH: 370

TYPE: PRT

ORGANISM: Homo Sapiens

US-10-753-267-86

Search completed: February 9, 2006, 01:21:15

Job time : 118.5 secs

Query Match 24.8%; Score 401; DB 5; Length 370;

Best Local Similarity 34.1%; Pred. No. 4.1e-30;

Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYGLVLLVGLLLSLALWFCRQQWQWTTETIYMTNLAVADICLLCTLPF-VLHSLR-- 81

Db 44 AVYVVVFLGLITNSVSLVFCFRMKMRSETAIFTNLAVSDLLFVCTLPFKIFYNFRH 103

QY 82 -DTSPTPLCOLSQGIYLTNRNYSISLVTAIVAVVHPLRAGLSRPROAAVCAVL 140

Db 104 WPFQGT-LCKISGTAPLTNIYSGMLFLTCISVDRFLAIVYPRRTIRNRSAIVCAGV 162

QY 141 WVLVIGSLVARWLLGQIE-----GGFCFRSTRHNFSNMR--PPLIGFYLP LAVVVF 189

Db 163 WILVLSGGISASLFPSTNNVNTTTCFEGFSKRVKTKYLSKITIEVVGVFIPLILNVS 222

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2006, 01:17:29 ; Search time 10.5 Seconds
(without alignments)
386.178 Million cell updates/sec

Title: US-10-083-168-85

Perfect score: 1615

Sequence: 1 MNGTYTCGSSDLTPPAIK.....AVAPRAKHSQDSLCVTLA 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/1/pubaa/US08 NEW PUB.pap.*
- 2: /cgn2_6/ptodata/1/pubaa/US06 NEW PUB.pap.*
- 3: /cgn2_6/ptodata/1/pubaa/US07 NEW PUB.pap.*
- 4: /cgn2_6/ptodata/1/pubaa/PCT NEW PUB.pap.*
- 5: /cgn2_6/ptodata/1/pubaa/US09 NEW PUB.pap.*
- 6: /cgn2_6/ptodata/1/pubaa/US10 NEW PUB.pap.*
- 7: /cgn2_6/ptodata/1/pubaa/US11 NEW PUB.pap.*
- 8: /cgn2_6/ptodata/1/pubaa/US60 NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	329.5	20.4	254	US-10-055-877-248
2	329.5	20.4	254	US-10-055-877-327
3	329.5	20.4	254	US-10-055-877-340
4	329.5	20.4	254	US-10-055-877-346-83
5	316.5	19.6	346	US-11-157-930-2
6	315.5	19.5	365	US-10-055-877-545
7	311.5	19.3	391	US-11-127-877-52
8	300	18.6	259	US-10-055-877-225
9	300	18.6	259	US-10-055-877-237
10	298	18.5	339	US-11-157-930-4
11	298	18.5	367	US-11-157-930-6
12	297.5	18.4	358	US-11-127-877-66
13	296.5	18.4	373	US-11-127-877-46
14	286.5	17.7	352	US-10-055-877-523
15	286.5	17.7	352	US-11-068-686-2
16	286.5	17.7	352	US-11-127-877-61
17	285.5	17.7	352	US-11-068-686-20
18	273.5	16.9	337	US-11-157-930-5
19	273.5	16.9	375	US-11-127-877-67
20	261.5	16.2	374	US-11-127-877-62
21	255.5	15.8	359	US-10-055-877-712
22	255.5	15.8	359	US-10-055-877-716
23	255.5	15.8	359	US-10-055-877-716
24	255.5	15.8	359	US-11-127-877-65
25	255.5	15.8	388	US-10-055-877-713

Sequence 714, App
Sequence 715, App
Sequence 55, Appl
Sequence 934, App
Sequence 838, App
Sequence 837, App
Sequence 2, Appli
Sequence 60, Appl
Sequence 161, App
Sequence 4, Appli
Sequence 64, Appl
Sequence 4, Appl
Sequence 36, Appl
Sequence 12, Appl
Sequence 24, Appl
Sequence 636, App
Sequence 637, App
Sequence 6, Appli
Sequence 59, Appl
Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-10-055-877-248
Sequence 248, Application US/10055877
Publication No. US20050289241A1

GENERAL INFORMATION:

APPLICANT: Decristofaro, Marc
APPLICANT: Padigar, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Ratelli, Luca
APPLICANT: Kekuda, Ramesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zerhusen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Patturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Eissen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shimketa, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Vernet, Corine
APPLICANT: Taupier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ferenc
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25


```

; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 340
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 7tm 1, 7
; OTHER INFORMATION: transmembrane receptor domain consensus sequence
US-10-055-877-340

Query Match 20.4%; Score 329.5; DB 6; Length 254;
Best Local Similarity 33.7%; Pred. No. 9.5e-25;
Matches 91; Conservative 54; Mismatches 88; Indels 37; Gaps 9;

Qy 28 GVLAVGLLNSLALVWFCRRQQWTEIRYVNTNLAVADLCCLCTL-PPVLHSLRD---T 83
Db 1 GNLLVILVILTKU-----RTPNIFILNLAVADLLFLFLTPPWLALYLVGGDWV 51

; SEQUENCE 83, Application US/10877346
; Publication No. US20060014153A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 7
; OTHER INFORMATION: transmembrane receptor Consensus Sequence
US-10-877-346-83

Qy 84 SDTFLCOLSQIYLTNRYMSISLVTAIAVDYVAVRHPRLRARGLSRQAAAVCAVLWVL 143
Db 52 FGDALCKLVGALFVWNGYASILLTALSIDRYLAIVHPLRVYRIRTPRAKVLILLVWVL 111
Qy 144 V-----TGSIVARMLGLQEGG-----FCFRSTRHNFNSMRPFLGLFYPLAVVVCSL 192
Db 112 ALLLSPLPLFLSWLRTVEGNTTVCLLIDFPPEESVKRSY-VLLSTLVGFVLPPLLVILVCYT 170
Qy 193 KVVTAQAORPPTDVG---QAEATRKAKRMVWVANLLVFVWCFPLPLHVLGTLVRLAVGMNACA 249
Db 171 RIILTKRARSQSRLKRRSSERKAKMLVVVVVFLVWVFLVWVFLVWVFLVWVFLVWVFLVWVFL 224
Qy 250 LLETIR---RALYITSKLSKDANCLDAICY 276
Db 225 LLSIWRVLPALTLITLWLVAVNSCLNPIY 254

RESULT 4
US-10-877-346-83
; Sequence 83, Application US/10877346
; Publication No. US20060014153A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 7
; OTHER INFORMATION: transmembrane receptor Consensus Sequence
US-10-877-346-83
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US-10-877-346-83

Query Match 20.4%; Score 329.5; DB 6; Length 254;
Best Local Similarity 33.7%; Pred. No. 9.5e-25;
Matches 91; Conservative 54; Mismatches 88; Indels 37; Gaps 9;

QY 28 GVLLVGLLLSLALVFCRCMQMTETRYMTNLAVADCLLCTL-PPVLSLRD---T 83
DB 1 GNLLVTLVTLTKK-----RPTNIFLNLAVADLLFLTLPPWALYLVGGDWV 51
QY 84 SDTFLCQLSQGIYLTNRYSISLVTAIAVDVAVVRHPLRARGLSPROAAAACAVLWVL 143
DB 52 PGDALCKLVAGLVNNGYASILLTALSIDRLAIVHPLRYRIRTPRAKVLILLWVL 111
QY 144 V-----IGSLVARWLLGIQGG-----PCFSTRNRNFMSPFLPGFYPLAVVVFCSL 192
DB 112 ALLSLPPLFLFWLRTVEBNTVCLIDPPESVKRSY-VLLSTLVGFVPLLVLCVYT 170
QY 193 KVVTAQAQRPPTDVG---QAEATRKAKRMVWNLVVFVCPFLPHVGLTVRLAVGNACA 249
DB 171 RLRLTLRKARSORSKRSSSRKAOKMLLVVVVFLCWLPHYHVL-----DSL 224
QY 250 LLETIR---RALYITSKLSDANCCDAICY 276
DB 225 LLSIRVLPALTLLWLVNLSCLNPIY 254

RESULT 5

US-11-157-930-2
; Sequence 2, Application US/11157930
; Publication No. US20050266482A1
; GENERAL INFORMATION:
; APPLICANT: Xieo, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/11/157,930
; PRIOR FILING DATE: 2005-06-22
; PRIOR APPLICATION NUMBER: US/09/828,478
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-157-930-2

Query Match 19.6%; Score 316.5; DB 7; Length 346;
Best Local Similarity 28.4%; Pred. No. 2.4e-23;
Matches 89; Conservative 64; Mismatches 139; Indels 21; Gaps 10;

QY 2 NGTYTCGSSDLTPWPAIKGY--AYGLVLLVGLLLSLALVFCRCMQMTETRYM 59
DB 20 NOTFSNNRNCT-IENFKREFPIVYL-IIFFWGLVGLNGLSIYVFLQPKKSTSVNFM 77
QY 60 TNLAVADCLLCTLP-VLHSLRDS-----DFPLCQLSQGIYLTNRYSISLVTAIADR 114
DB 78 LNLASDLLFISTLPFRADYLRGNSWIFGDLACRIMSLSLV-NMYSIYFLTVLSVR 136
QY 115 YVAVRPLRARGLSRPROAAAACAVLWLVIGSLVARWLLGIQGG---PCFSTRNRNFM 171
DB 137 FLAWVHPFLHVTIERSAWICGIIWILIMASSIMLLDSGSEQSGVTSCELMNLYKIA 196
QY 172 SMRFP-----LLGYPLPLAVVVFCSLKVVTAQAQRPPTDVQAEATRKAKRMVWNLV 226
DB 197 KLQTMNIALVVGCLPPFTLSICVLLIIRVLLKVEPESGLRVSHRKALITIIITLIIF 256
QY 227 VVCPFLPHVGLTVRLAVGNACALLETIRRALYITSKLSDANCCDAICYMAKEPQB- 285

Db 257 FLCFLPYHTLRTVHLTT-WKVGCLCKRHLKALVITLALAAANACFNPLLYTFAGENFKDR 315
QY 286 -ASALAVAPRAKA 297
DB 316 LKSALRKGGHPQKA 328

RESULT 6
US-10-995-561-545
; Sequence 545, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 545
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-545

Query Match 19.5%; Score 315.5; DB 6; Length 365;
Best Local Similarity 29.2%; Pred. No. 3.2e-23;
Matches 94; Conservative 56; Mismatches 123; Indels 49; Gaps 12;

QY 29 VLLVGLLLSLALVFCRCMQMTETRYMTNLAVADCLLCTLPFLVHSLRDTSDTP- 87
DB 44 VVFLVGLGLNAPTLWLFIFRLRPWDATATYMFHLASDTLVLSLPTLIYYAAHNPFP 103
QY 88 ---LCQLSQGIYLTNRYSISLVTAIAVDVAVVRHPLRARGLSRPROAAAACAVLWVL 144
DB 104 GTEICKFVRFLFYWNLYCSVLFTCISVHRYLGICHPRLALRWGRPRLAGLLCLAVLWV 163
QY 145 IGSILVAR-WLGIQGG---PCFSTR-----H--NFSNRPFLGFLVPLAVVVFCSLK 193
DB 164 AGCLVNLFFVTTNKGTTVLCHDTTPEEDPHVHFSSAVMGLL-FQVPCLVTLVCVGL 222
QY 194 VVTAQAQRPPTDVQAEATRKAK--RMVWNLVVFVVCFLPHVGLTV-----RLAVGMA 247
DB 223 MARLYQPLP---GSAQSSRLSLRTIAVVLTVFAVCFVPHITRTIYYLARLEA--D 277
QY 248 CALLETIRRALYITSKLSDANCCDAICYMAKEPQB-----ASALAV 291
DB 278 CRVLNVVVVYKVRPLASANSCLDPVLYLTGDKYRRQLQLOGGKGPQPRTAASSLAL 337
QY 292 APRAK-----AHKSQDSLCVT 307
DB 338 VSLPEDSSCRWAATPQDSSCST 359

RESULT 7

US-11-127-877-52
; Sequence 52, Application US/11127877
; Publication No. US2005028756SA1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann, Pascal G.
; APPLICANT: Merckhans, Marcel
; APPLICANT: Spittaels, Koenraad P. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12

```

; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-52

Query Match      19.3%; Score 311.5; DB 7; Length 391;
Best Local Similarity 27.6%; Pred. No. 8.3e-23;
Matches 89; Conservative 54; Mismatches 128; Indels 51; Gaps 9;

Qy 1 MNGTYNTCGSDLTW-----PPAIGLGFYAVLGVLLVGLLNSIALWVFCRCMQW 52
Db 38 LMGTFQSKCPQVWGLWNTIQPP-----FLWVLFVLATLENIFVLSVFCILHKSSC 89

Qy 53 TETRIYMTNLAVADCLLCTLPFVHLSDTSD----TPLCQLSQGIYLTNRYSISLVT 108
Db 90 TVAEIYIGNLAADULLIACGLFPFWAITISNFDWLFGETLCRVVNAISNNLYSSICFLM 149

Qy 109 AIAVDYVAVRHLRLRGLRSPROAAVCAVLW--VLVIGS--LVARWLLGIQGGFCFR 164
Db 150 LVSIDRYLALVKTWSMGRGVRWAKLYSLVINGCTLLSSPMLVFRMTKEYSDEG--- 205

Qy 165 STRIN-----FNSRFPPLGFLYPLAVVVFCSLKVVTALAQRPPTDVGOA 209
Db 206 ---HNVTACVISYPSLIWEVETNMLNVLVGVFLPLSVITFTQMIOVLRNEMQKPKFI 262

Qy 210 EATRKAKRWANLIVFVVCFLPLHVLTV---RLAVGNWACALLETTIRRALYITSKLS 265
Db 263 QTERATVILVVLVLLFFLICMLPFQISTFTDLTLRLGI-LSSCQDERIIDVITQJASFMA 321

Qy 266 DANCCLDAICYNNMAKFEQAS 287
Db 322 YSNSCLNPLVTVIVGKFRKKS 343

RESULT 8
US-10-055-877-225
; Sequence 225, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Rattelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taulier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference

; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 225
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 7tm_1 domain
; OTHER INFORMATION: consensus sequence
US-10-055-877-225

Query Match      18.6%; Score 300; DB 6; Length 259;
Best Local Similarity 32.6%; Pred. No. 6.8e-22;
Matches 92; Conservative 49; Mismatches 85; Indels 56; Gaps 10;

Qy 28 GVLVLGLLNSLALWVFCRCMQWETRIYMTNLAVADCLLCTLPFVHLSDTSD- 85
Db 1 GNLVLVILVILRTKKL-----RTPTNIFILNLAVALDLFLTLPPWALYLVGGSED 51

Qy 86 ---TPLCQLSQGIYLTNRYSISLVTAVDVAVRHLRLRGLR-SPROAAVCAVL 140
Db 52 WPFGLSALCKLVTDVDDVNMVNASILLTAISIDRYLAVHPLRYRRRTSPRAKVILLV 111

Qy 141 WVLV----IGSLVARWLLGIQEGG-----FCFRSTRHNFNSMR-----FPLL 178
Db 112 WVLALLSLPLLPFLFSWKTVEEGNTLVNVVTVCLIDFPPEBSTASVSTWLSYVLLSTLV 171

Qy 179 GFYLPVAVVVFCSLKVVTALAQRPPTDVGOAEATRKAKRWANLIVFVVCFLPHVGL- 237
Db 172 GFLLPLLVILVCYTRILRTL-----RKAATLLVWVWVFLVCLWLPYFIVLL 217

Qy 238 ---TVRLAVGNWA-CALLETTIRRALYITSKLSDANCCCLDAICY 276
Db 218 LDTLCLSIIMSSTCELSERVLPFTALLVTLWLAIVNSCLNPIIY 259

RESULT 9
US-10-055-877-237
; Sequence 237, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
```


Query Match 18.4%; Score 297.5; DB 7; Length 358;
Best Local Similarity 29.4%; Pred. No. 1.7e-21;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 01:16:44 ; Search time 118.5 Seconds
(without alignments)
1089.530 Million cell updates/sec

Title: US-10-083-168-16
Perfect score: 1614
Sequence: 1 MNGTYNTCGSSDLTPPAIK.....AVAPRAKAHKSQDSLCVTLA 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1614	100.0	309	US-09-768-877-20	Sequence 20, Appl
2	1614	100.0	309	US-10-225-567A-492	Sequence 492, App
3	1614	100.0	309	US-10-696-639-44	Sequence 44, Appl
4	1608	99.6	547	US-10-505-486-84	Sequence 84, Appl
5	1602	99.3	309	US-10-157-031-351	Sequence 351, App
6	402	24.9	370	US-09-964-821B-11	Sequence 11, Appl
7	402	24.9	370	US-10-081-810-44	Sequence 44, Appl
8	402	24.9	370	US-10-225-567A-225	Sequence 225, App
9	402	24.9	370	US-10-024-298A-176	Sequence 176, App
10	402	24.9	370	US-10-042-211A-176	Sequence 176, App
11	402	24.9	370	US-10-268-332-11	Sequence 11, Appl
12	402	24.9	370	US-10-617-217A-176	Sequence 176, App
13	402	24.9	370	US-10-775-965-11	Sequence 11, Appl
14	402	24.9	370	US-10-024-298A-176	Sequence 176, App
15	402	24.9	370	US-10-753-267-86	Sequence 86, Appl
16	402	24.9	608	US-10-505-486-114	Sequence 114, App
17	401	24.8	370	US-09-964-821B-10	Sequence 10, Appl
18	401	24.8	370	US-10-268-332-10	Sequence 10, Appl
19	392	24.3	370	US-10-024-298A-174	Sequence 174, App
20	392	24.3	370	US-10-042-211A-174	Sequence 174, App
21	392	24.3	370	US-10-617-217A-174	Sequence 174, App
22	392	24.3	370	US-10-024-298A-174	Sequence 174, App
23	390	24.2	368	US-10-775-965-10	Sequence 10, Appl
24	381.5	23.6	363	US-10-314-048A-159	Sequence 159, App
25	381.5	23.6	363	US-10-897-815-159	Sequence 159, App
26	381.5	23.6	363	US-10-930-662-159	Sequence 159, App
27	376.5	23.3	363	US-09-930-334-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-768-877-20
; Sequence 20, Application US/09768877
; Patent No. US20020150896A1
; GENERAL INFORMATION:
; APPLICANT: POLONSKY, KENNETH S.
; APPLICANT: HORIKAWA, YUKIO
; APPLICANT: ODA, NAOHISA
; APPLICANT: COX, NANCY J.
; APPLICANT: SRENNAN, SEAMUS
; APPLICANT: ZHOU, YUN-PING
; APPLICANT: OTANI, KENICHI
; APPLICANT: HANIS, CRAIG L.
; APPLICANT: BELL, GRAEME I.
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
; FILE REFERENCE: ARCD:307
; CURRENT APPLICATION NUMBER: US/09/768,877
; CURRENT FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 09/422,869
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Human
US-09-768-877-20

Query Match 100.0%; Score 1614; DB 3; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 16, Appl
Sequence 1, Appl
Sequence 4, Appl
Sequence 54202, A
Sequence 45, Appl
Sequence 36, Appl
Sequence 226, App
Sequence 668, App
Sequence 36, Appl
Sequence 36, Appl
Sequence 14, Appl
Sequence 36, Appl
Sequence 4, Appl
Sequence 766, App
Sequence 2, Appl
Sequence 808, App
Sequence 12, Appl

QY 1 MNGTYNTCGSSDLTPPAIKLGFYALVGLVLLGLLNSLALWVFCRCMQQWTEIYMT 60
DB 1 MNGTYNTCGSSDLTPPAIKLGFYALVGLVLLGLLNSLALWVFCRCMQQWTEIYMT 60
QY 61 NLAVADLCLLCTLPFVLSLRDTSDFLQSLQGIYLTNRYSISLVTIAVDYVAVRH 120
DB 61 NLAVADLCLLCTLPFVLSLRDTSDFLQSLQGIYLTNRYSISLVTIAVDYVAVRH 120
QY 121 PLRARGLRSPROAAVCAVLVWVLSVARMILQEGGFCFRSTRHNSRFPLLGF 180
DB 121 PLRARGLRSPROAAVCAVLVWVLSVARMILQEGGFCFRSTRHNSRFPLLGF 180
QY 181 YLPLAVVVFCSLKVVVTAQAORPPTDVQAEATKAAWYVWNLVFWVCFPLHVLGTVR 240
DB 181 YLPLAVVVFCSLKVVVTAQAORPPTDVQAEATKAAWYVWNLVFWVCFPLHVLGTVR 240
QY 241 LAVGWNACALLETIRRALYITSKLSDANCCLDAICYIYMAKEFQEASALAVAPRAKAHKS 300

Db 241 LAVGNACALLETIRRALYITISKLSANDCCCLDAICYNNMAKEFQASALAVAPRAKAHKS 300

Qy 301 QDSLVCVTLA 309
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Db 301 QDSLVCVTLA 309

RESULT 2

US-10-225-567A-492

; Sequence 492, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burner, Joseph C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 492

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-225-567A-492

Query Match 100.0%; Score 1614; DB 4; Length 309;

Best Local Similarity 100.0%; Pred. No. 1.2e-145;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNGTYNTCGSSDLTPWPPAIKLGFYALGVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
|||||

Db 1 MNGTYNTCGSSDLTPWPPAIKLGFYALGVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
|||||

Qy 61 NLAVADLCCLCTLPFVLSLRDTSPTPLCQSQGIYLTNRYSISLVTIAVDRYVAVRH 120
|||||

Db 61 NLAVADLCCLCTLPFVLSLRDTSPTPLCQSQGIYLTNRYSISLVTIAVDRYVAVRH 120
|||||

Qy 121 PLRARGLSRPROAAAACAVLWVLSVARWLLGIQGGFCFRSTRHFNFSMRPPLIGF 180
|||||

Db 121 PLRARGLSRPROAAAACAVLWVLSVARWLLGIQGGFCFRSTRHFNFSMRPPLIGF 180
|||||

Qy 181 YLPLAVVVFCSLVKVTALAQRPTDVGOAETKKAARMVWVANLLVFVVCFLPLHVGLTVR 240
|||||

Db 181 YLPLAVVVFCSLVKVTALAQRPTDVGOAETKKAARMVWVANLLVFVVCFLPLHVGLTVR 240
|||||

Qy 241 LAVGNACALLETIRRALYITISKLSANDCCCLDAICYNNMAKEFQASALAVAPRAKAHKS 300
|||||

Db 241 LAVGNACALLETIRRALYITISKLSANDCCCLDAICYNNMAKEFQASALAVAPRAKAHKS 300
|||||

Qy 301 QDSLVCVTLA 309
|||||

Db 301 QDSLVCVTLA 309

RESULT 3

US-10-696-639-44

; Sequence 44, Application US/10696639

; Publication No. US20050037439A1

; GENERAL INFORMATION:

; APPLICANT: Pharmacia Corporation

; APPLICANT: Bourner, Maureen J.

; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE

; FILE REFERENCE: 01040/1

; CURRENT APPLICATION NUMBER: US/10/696,639

; CURRENT FILING DATE: 2003-10-29

; PRIOR APPLICATION NUMBER: 60/422,176

; PRIOR FILING DATE: 2002-10-29

Qy 241 LAVGNACALLETIRRALYITISKLSANDCCCLDAICYNNMAKEFQASALAVAPRAKAHKS 300
|||||

Db 241 LAVGNACALLETIRRALYITISKLSANDCCCLDAICYNNMAKEFQASALAVAPRAKAHKS 300
|||||

Qy 301 QDSLVCVTLA 309
|||||

Db 301 QDSLVCVTLA 309

Query Match 99.6%; Score 1608; DB 5; Length 547;

Best Local Similarity 99.7%; Pred. No. 8.4e-145;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNGTYNTCGSSDLTPWPPAIKLGFYALGVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
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Db 1 MNGTYNTCGSSDLTPWPPAIKLGFYALGVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
|||||

Qy 61 NLAVADLCCLCTLPFVLSLRDTSPTPLCQSQGIYLTNRYSISLVTIAVDRYVAVRH 120
|||||

Db 61 NLAVADLCCLCTLPFVLSLRDTSPTPLCQSQGIYLTNRYSISLVTIAVDRYVAVRH 120
|||||

Qy 121 PLRARGLSRPROAAAACAVLWVLSVARWLLGIQGGFCFRSTRHFNFSMRPPLIGF 180
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; NUMBER OF SEQ ID NOS: 3114

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 44

; LENGTH: 309

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-696-639-44

Query Match 100.0%; Score 1614; DB 5; Length 309;

Best Local Similarity 100.0%; Pred. No. 1.2e-145;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNGTYNTCGSSDLTPWPPAIKLGFYALGVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
|||||

Db 1 MNGTYNTCGSSDLTPWPPAIKLGFYALGVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
|||||

Qy 61 NLAVADLCCLCTLPFVLSLRDTSPTPLCQSQGIYLTNRYSISLVTIAVDRYVAVRH 120
|||||

Db 61 NLAVADLCCLCTLPFVLSLRDTSPTPLCQSQGIYLTNRYSISLVTIAVDRYVAVRH 120
|||||

Qy 121 PLRARGLSRPROAAAACAVLWVLSVARWLLGIQGGFCFRSTRHFNFSMRPPLIGF 180
|||||

Db 121 PLRARGLSRPROAAAACAVLWVLSVARWLLGIQGGFCFRSTRHFNFSMRPPLIGF 180
|||||

Qy 181 YLPLAVVVFCSLVKVTALAQRPTDVGOAETKKAARMVWVANLLVFVVCFLPLHVGLTVR 240
|||||

Db 181 YLPLAVVVFCSLVKVTALAQRPTDVGOAETKKAARMVWVANLLVFVVCFLPLHVGLTVR 240
|||||

Qy 241 LAVGNACALLETIRRALYITISKLSANDCCCLDAICYNNMAKEFQASALAVAPRAKAHKS 300
|||||

Db 241 LAVGNACALLETIRRALYITISKLSANDCCCLDAICYNNMAKEFQASALAVAPRAKAHKS 300
|||||

Qy 301 QDSLVCVTLA 309
|||||

Db 301 QDSLVCVTLA 309

RESULT 4

US-10-505-486-84

; Sequence 84, Application US/10505486

; Publication No. US20050118639A1

; GENERAL INFORMATION:

; APPLICANT: Takeda Chemical Industries, Ltd.

; TITLE OF INVENTION: Determination of a ligand

; FILE REFERENCE: P03-0006PCT

; CURRENT APPLICATION NUMBER: US/10/505,486

; CURRENT FILING DATE: 2004-08-20

; PRIOR APPLICATION NUMBER: JP 2002-45728

; PRIOR FILING DATE: 2002-02-22

; PRIOR APPLICATION NUMBER: JP 2002-213949

; PRIOR FILING DATE: 2002-07-23

; PRIOR APPLICATION NUMBER: JP 2002-298237

; PRIOR FILING DATE: 2002-10-11

; NUMBER OF SEQ ID NOS: 233

; SEQ ID NO 84

; LENGTH: 547

; TYPE: PRT

; ORGANISM: Human

US-10-505-486-84

Query Match 99.6%; Score 1608; DB 5; Length 547;

Best Local Similarity 99.7%; Pred. No. 8.4e-145;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNGTYNTCGSSDLTPWPPAIKLGFYALGVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
|||||

Db 1 MNGTYNTCGSSDLTPWPPAIKLGFYALGVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
|||||

Qy 61 NLAVADLCCLCTLPFVLSLRDTSPTPLCQSQGIYLTNRYSISLVTIAVDRYVAVRH 120
|||||

Db 61 NLAVADLCCLCTLPFVLSLRDTSPTPLCQSQGIYLTNRYSISLVTIAVDRYVAVRH 120
|||||

Qy 121 PLRARGLSRPROAAAACAVLWVLSVARWLLGIQGGFCFRSTRHFNFSMRPPLIGF 180
|||||

Db 121 PLRARGLRSPQAAAVCAVLVVLVIGSLVARWLLGIQSGGCFRSTRHFNFSMAFPLLG 180
Qy 181 YLPLAVVFCSLKVVTALAQRPPTDVGAETRKAARMVWNLVVFVCFPLPHVGLTVR 240
Db 181 YLPLAVVFCSLKVVTALAQRPPTDVGAETRKAARMVWNLVVFVCFPLPHVGLTVR 240
Qy 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKAHS 300
Db 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKAHS 300
Qy 301 QDSLVCVTLA 309
Db 301 QDSLVCVTLA 309

RESULT 5

US-10-157-031-351
; Sequence 351, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 351
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-351

Query Match 99.3%; Score 1602; DB 4; Length 309;
Best Local Similarity 99.4%; Pred. No. 1.6e-144;
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNGTYNTCGSSDLTPWPAIKLGFYALGVLLVIGLLNLSLALWVFCRMOQWTTETRIYMT 60
Db 1 MNGTYNTCGSSDLTPWPAIKLGFYALGVLLVIGLLNLSLALWVFCRMOQWTTETRIYMT 60
Qy 61 NLAVADLCLLCTLPFVHLSRDTSDTPLCQLSQGIYLTNRYSISLVTALVDRYVAVRH 120
Db 61 NLAVADLCLLCTLPFVHLSRDTSDTPLCQLSQGIYLTNRYSISLVTALVDRYVAVRH 120
Qy 121 PLRARGLRSPQAAAVCAVLVVLVIGSLVARWLLGIQSGGCFRSTRHFNFSMAFPLLG 180
Db 121 PLRARGLRSPQAAAVCAVLVVLVIGSLVARWLLGIQSGGCFRSTRHFNFSMAFPLLG 180
Qy 181 YLPLAVVFCSLKVVTALAQRPPTDVGAETRKAARMVWNLVVFVCFPLPHVGLTVR 240
Db 181 YLPLAVVFCSLKVVTALAQRPPTDVGAETRKAARMVWNLVVFVCFPLPHVGLTVR 240
Qy 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKAHS 300
Db 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKAHS 300
Qy 301 QDSLVCVTLA 309
Db 301 QDSLVCVTLA 309

RESULT 6

US-09-964-821B-11
; Sequence 11, Application US/09964821B
; Publication No. US20030186360A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J. N.

; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C. S.
; APPLICANT: HAWKEN, D.R.
; APPLICANT: CACACE, A.
; APPLICANT: BARBER, L.
; APPLICANT: KORNACKER, M. G.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV3,
; TITLE OF INVENTION: EXPRESSED HIGHLY IN IMMUNE- AND COLON- RELATED TISSUES
; FILE REFERENCE: D0042NP
; CURRENT APPLICATION NUMBER: US/09/964,821B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,783
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/305,085
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/313,171
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-821B-11

Query Match 24.9%; Score 402; DB 3; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

Qy 25 AVLGVLLVIGLLNLSLALWVFCRMOQWTTETRIYMTNLAVADLCLLCTLPF-VLHSLR-- 81
Db 44 AVYSVVFILGHTNSVLSLFCFRKMKRSETAFTINLAVSDLLFVCTLPFKIFYNFNRH 103
Qy 82 -DTSPTPLCQLSQGIYLTNRYSISLVTALVDRYVAVRHPLRARGLRSPQAAAVCAVL 140
Db 104 WPFQGT-LCKISGTAFTLNIYGSMLFTCISVDRELAIVYPPRSRTIRTRNSAIVCAGV 162
Qy 141 WLVVIGSLVARWLLGIQSGGCFRSTRHFNFSNR--FPLLGFLVPLAVVVF 189
Db 163 WILVLSGISASLSTFTTNVNNATTCFEGFSKRWKTYLSKTIPIEVVGFIIPLINVS 222
Qy 190 CSLKVVTALAQRPPTDVGAETRKAARMVWNLVVFVCFPLPHVGLTVRLAVGNAC 248
Db 223 CSSVVRITL--RKPAITLSQIGTKKKKXLMITVHMAVFCVFPYNSVLFLVALVRSQAI 280
Qy 249 --ALLETIRRALY-ITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKAHSQDSL 305
Db 281 TNCFLERFAKIMYPITLCLATLNCDFPFIYVFTLESFQKSFYI-----NAHIRMESLP 334
Qy 306 VT 307
Db 335 KT 336

RESULT 7

US-10-081-810-44
; Sequence 44, Application US/10081810
; Publication No. US20030064438A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR NUCLEIC ACIDS, POLYPEPTIDES, ANTIBODI
; FILE REFERENCE: D0132 NP
; CURRENT APPLICATION NUMBER: US/10/081,810
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: US 60/270,793
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/270,792
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/296,427
; PRIOR FILING DATE: 2001-06-06

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; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-081-810-44

Query Match      24.9%; Score 402; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVGLLNSLALWFCRMOQWTEIRYMTNLAVADICLLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVSLVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFPNRHH 103
QY 82 -DTSDFPLCOLSQGIYLTNRNYSISLVTAIVDRYVAVRHPLRARGLRSPROAAAVCAVL 140
DB 104 WPFQDT-LCKISGTAFITNIGSMFLTCISVDRFLAIVYPPFRSRTIRTRNSAIVCAGV 162
QY 141 WVLVIGSLVARWLLGIQEQ-----GGCFRSTRHNFSMR--PPLLGFYPLAVVVVF 189
DB 163 WILVSGGISASLFSSTNNVNNATTCFEGFSKRVKMTYLSKITIFIEVVGFIPIILNVS 222
QY 190 CSLKVVTAQAORPPTDVGQAEAT-RKAARMVWVANLLVVFVCFPLPLHVLGTVRLAVGWNAC 248
DB 223 CSSVVLRTL--RKPAITLSQIGTNKKKVLKMITVHMAVVFVCFVFNYSVLFYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSDANCCLDALCYIYMAKEFOEASALAVAPRAKAHKSQDSL 305
DB 281 TNCFLERPAKIMYPITCLATLNCDFPFIYFTLESFQKSPYI-----NAHIRMESLF 334
QY 306 VT 307
DB 335 KT 336

RESULT 8
US-10-225-567A-225
; Sequence 225, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 225
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-225

Query Match      24.9%; Score 402; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVGLLNSLALWFCRMOQWTEIRYMTNLAVADICLLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVSLVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFPNRHH 103
QY 82 -DTSDFPLCOLSQGIYLTNRNYSISLVTAIVDRYVAVRHPLRARGLRSPROAAAVCAVL 140
DB 104 WPFQDT-LCKISGTAFITNIGSMFLTCISVDRFLAIVYPPFRSRTIRTRNSAIVCAGV 162
QY 141 WVLVIGSLVARWLLGIQEQ-----GGCFRSTRHNFSMR--PPLLGFYPLAVVVVF 189
DB 163 WILVSGGISASLFSSTNNVNNATTCFEGFSKRVKMTYLSKITIFIEVVGFIPIILNVS 222
QY 190 CSLKVVTAQAORPPTDVGQAEAT-RKAARMVWVANLLVVFVCFPLPLHVLGTVRLAVGWNAC 248
DB 223 CSSVVLRTL--RKPAITLSQIGTNKKKVLKMITVHMAVVFVCFVFNYSVLFYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSDANCCLDALCYIYMAKEFOEASALAVAPRAKAHKSQDSL 305
DB 281 TNCFLERPAKIMYPITCLATLNCDFPFIYFTLESFQKSPYI-----NAHIRMESLF 334
QY 306 VT 307
DB 335 KT 336

RESULT 9
US-10-024-298A-176
; Sequence 176, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP008912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-176

Query Match      24.9%; Score 402; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVGLLNSLALWFCRMOQWTEIRYMTNLAVADICLLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVSLVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFPNRHH 103
QY 82 -DTSDFPLCOLSQGIYLTNRNYSISLVTAIVDRYVAVRHPLRARGLRSPROAAAVCAVL 140
DB 104 WPFQDT-LCKISGTAFITNIGSMFLTCISVDRFLAIVYPPFRSRTIRTRNSAIVCAGV 162
QY 141 WVLVIGSLVARWLLGIQEQ-----GGCFRSTRHNFSMR--PPLLGFYPLAVVVVF 189
DB 163 WILVSGGISASLFSSTNNVNNATTCFEGFSKRVKMTYLSKITIFIEVVGFIPIILNVS 222
QY 190 CSLKVVTAQAORPPTDVGQAEAT-RKAARMVWVANLLVVFVCFPLPLHVLGTVRLAVGWNAC 248
DB 223 CSSVVLRTL--RKPAITLSQIGTNKKKVLKMITVHMAVVFVCFVFNYSVLFYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSDANCCLDALCYIYMAKEFOEASALAVAPRAKAHKSQDSL 305
DB 281 TNCFLERPAKIMYPITCLATLNCDFPFIYFTLESFQKSPYI-----NAHIRMESLF 334
QY 306 VT 307
DB 335 KT 336
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-217A-176

Query Match      24.9%; Score 402; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVLLGLLNSLALWVFCRMOQWETRIYMTNLAVADCLLCTLPF-VLHSLR-- 81
Db 44 AVYSVVFILGLITNSVSLVFCFRMKMRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
QY 82 -DTSPTPLCQLSQGIYLTNRYSISLVTAIVDRYVAVRHPLRARGLRSPRQAAACAVL 140
Db 104 WPFQDT-LCKISGTAFITNIYGMFLFTCISVDRLAIVYPPFRSRTIRTRNSAIVCAGV 162
QY 141 WLVIGSLVARWLLGQEQ-----GGFCFRSTRHNFSMR--PPLLGFLYPLAVVVF 189
Db 163 WILVLSGGISASLFTSTNNVNAATTCFEGFSKRWKTYLSKITIFIEVVGFIPLILNVS 222
QY 190 CSLKVVVTTALAQRPPTDVGQAEAT-RKAARMVMANLLVFVVCFLPLHLVGLTVRLAVGWNAC 248
Db 223 CSSVVLRTL--RKPATLSQIGTKKKVLMKMTVHMAVFCVFPVNSVLFYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSANDCCLDALCIYYMAKEFOEASALAVAPRAKAHKSQDSL 305
Db 281 TNCFLERPAKIMYPITCLATLNCDFPFIYYFTLESFQKSFYI-----NAHIRMESLF 334
QY 306 VT 307
Db 335 KT 336

RESULT 14
US-10-024-298A-176
; Sequence 176, Application US/10024298A
; Publication No. US20040214167A9
; GENERAL INFORMATION:
; APPLICANT: ASAH KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NP-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-176

Query Match      24.9%; Score 402; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVLLGLLNSLALWVFCRMOQWETRIYMTNLAVADCLLCTLPF-VLHSLR-- 81
Db 44 AVYSVVFILGLITNSVSLVFCFRMKMRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
QY 82 -DTSPTPLCQLSQGIYLTNRYSISLVTAIVDRYVAVRHPLRARGLRSPRQAAACAVL 140
Db 104 WPFQDT-LCKISGTAFITNIYGMFLFTCISVDRLAIVYPPFRSRTIRTRNSAIVCAGV 162
QY 141 WLVIGSLVARWLLGQEQ-----GGFCFRSTRHNFSMR--PPLLGFLYPLAVVVF 189
Db 163 WILVLSGGISASLFTSTNNVNAATTCFEGFSKRWKTYLSKITIFIEVVGFIPLILNVS 222
QY 190 CSLKVVVTTALAQRPPTDVGQAEAT-RKAARMVMANLLVFVVCFLPLHLVGLTVRLAVGWNAC 248
Db 223 CSSVVLRTL--RKPATLSQIGTKKKVLMKMTVHMAVFCVFPVNSVLFYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSANDCCLDALCIYYMAKEFOEASALAVAPRAKAHKSQDSL 305
Db 281 TNCFLERPAKIMYPITCLATLNCDFPFIYYFTLESFQKSFYI-----NAHIRMESLF 334
QY 306 VT 307
Db 335 KT 336

RESULT 13
US-10-775-965-11
; Sequence 11, Application US/10775965
; Publication No. US20040209808A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Kornacker, Michael
; TITLE OF INVENTION: MODULATORS OF HUMAN G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: D0286 NP
; CURRENT APPLICATION NUMBER: US/10/775,965
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: U.S. 60/446,655
; PRIOR FILING DATE: 2003-02-11
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-965-11

Query Match      24.9%; Score 402; DB 4; Length 370;
Best Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVLLGLLNSLALWVFCRMOQWETRIYMTNLAVADCLLCTLPF-VLHSLR-- 81
Db 44 AVYSVVFILGLITNSVSLVFCFRMKMRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
QY 82 -DTSPTPLCQLSQGIYLTNRYSISLVTAIVDRYVAVRHPLRARGLRSPRQAAACAVL 140
Db 104 WPFQDT-LCKISGTAFITNIYGMFLFTCISVDRLAIVYPPFRSRTIRTRNSAIVCAGV 162
QY 141 WLVIGSLVARWLLGQEQ-----GGFCFRSTRHNFSMR--PPLLGFLYPLAVVVF 189
Db 163 WILVLSGGISASLFTSTNNVNAATTCFEGFSKRWKTYLSKITIFIEVVGFIPLILNVS 222
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Qy 190 CSLKVVTTALQRPPTDVQAEAT-RKARMMWANLIVFVVCFLPLHVGLTVRLAVGNAC 248
Db 223 CSSVLRLL--RKPATLSQIGTNKKVLMITVHMAVVFVVCFFVYNSVLFYALVRSQAI 280
Qy 249 --ALLETTIRALY-ITSKLSDANCCCLDAICVYVMKEFOEASALAVAPRAKAKHSQDSLC 305
Db 281 TNCFLERFAKIMYPITICLATLNCDDFFIYFTLESFQKSFYI-----NAHIRMESLP 334
Qy 306 VT 307
Db 335 KT 336

Search completed: February 9, 2006, 01:21:15
Job time : 120.5 secs

Db 335 KT 336
US-10-753-267-86
; Sequence 86, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Stegiano, Nancy E.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Donoghue, Mary A.
; APPLICANT: Rodriguez-Way, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
; TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
; TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419
; FILE REFERENCE: MP103-003P1RNMIM
; CURRENT APPLICATION NUMBER: US/10/753,267
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/439,683
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/445,216
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,036
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/454,189
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/457,541
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/466,411
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/469,041
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/477,414
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/478,560
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/489,772
; PRIOR FILING DATE: 2003-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-753-267-86

Query Match 24.9%; Score 402; DB 5; Length 370;
Best-Local Similarity 34.1%; Pred. No. 8.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;
Qy 25 AYGLVLLVGLLINSIALWFCRMOQWTETRIYMTNLAVALDCLLCTLPF-VLHSLR-- 81
Db 44 AVSVVVFILGLITNSVSLVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
Qy 82 -DTSPTPLCQLSQGIYLTNRYSISLVAIAVDVYVVRHPLRARGLSRPROAAACAVL 140
Db 104 WPFQGT-LCKISTAFPLTNIYGSMLFLTCISVDRLAIVPFRSRTIRRRNSAIVCAGV 162
Qy 141 WLVIGSLVARMILGIQE-----GGFCFRSTRHNFNSMR--PPLLGFLPLAVVVF 189
Db 163 WLVLSGGISASLFSSTNNVNTTTCFEGFSKRVKWTLSKITIFIEVVGFIIPLNLVS 222

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OM protein - protein search, using sw model

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(without alignments)
386.178 Million cell updates/sec

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Perfect score: 1614
Sequence: 1 MNGTYNTCGSSDLTPPAIK.....AVAPRAKHSQDSLCTVLA 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 1312538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
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2: /cgm2_6/ptodata/1/pubpaa/US06 NEW PUB.pap.*
3: /cgm2_6/ptodata/1/pubpaa/US07 NEW PUB.pap.*
4: /cgm2_6/ptodata/1/pubpaa/PCT NEW PUB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	334.5	20.7	254	6	US-10-055-877-248 Sequence 248, App
2	334.5	20.7	254	6	US-10-055-877-327 Sequence 327, App
3	334.5	20.7	254	6	US-10-055-877-340 Sequence 340, App
4	334.5	20.7	254	6	US-10-055-877-346-83 Sequence 83, Appl
5	317.5	19.7	346	7	US-11-157-930-2 Sequence 2, Appli
6	315.5	19.5	365	6	US-10-995-561-545 Sequence 545, App
7	312.5	19.4	391	7	US-11-127-877-52 Sequence 52, Appl
8	305	18.9	259	6	US-10-055-877-225 Sequence 225, App
9	305	18.9	259	6	US-10-055-877-237 Sequence 237, App
10	300	18.6	339	7	US-11-157-930-4 Sequence 4, Appli
11	300	18.6	367	7	US-11-157-930-6 Sequence 6, Appli
12	298.5	18.5	373	7	US-11-127-877-46 Sequence 46, Appl
13	297.5	18.4	358	7	US-11-127-877-66 Sequence 66, Appl
14	288.5	17.9	352	6	US-10-995-561-523 Sequence 523, App
15	288.5	17.9	352	7	US-11-068-686-2 Sequence 2, Appli
16	288.5	17.9	352	7	US-11-127-877-61 Sequence 61, Appl
17	287.5	17.8	352	7	US-11-068-686-20 Sequence 20, Appl
18	275.5	17.1	337	7	US-11-157-930-5 Sequence 5, Appli
19	270.5	16.8	375	7	US-11-127-877-67 Sequence 67, Appl
20	263.5	16.3	374	7	US-11-127-877-62 Sequence 62, Appl
21	255.5	15.8	359	6	US-10-995-561-712 Sequence 712, App
22	255.5	15.8	359	6	US-10-995-561-716 Sequence 716, App
23	255.5	15.8	359	6	US-10-876-787-2 Sequence 2, Appli
24	255.5	15.8	359	7	US-11-127-877-65 Sequence 65, Appl
25	255.5	15.8	388	6	US-10-995-561-713 Sequence 713, App

Sequence 714, App
Sequence 715, App
Sequence 55, Appl
Sequence 934, App
Sequence 2, Appli
Sequence 838, App
Sequence 837, App
Sequence 161, App
Sequence 60, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 64, Appli
Sequence 36, Appli
Sequence 636, App
Sequence 637, App
Sequence 12, Appl
Sequence 24, Appl
Sequence 6, Appli
Sequence 59, Appl
Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-10-055-877-248
; Sequence 248 Application US/10055877
; Publication No. US2005028241A1

GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25

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; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 248
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 7tm_1, 7
; OTHER INFORMATION: transmembrane receptor domain
US-10-055-877-248

Query Match      20.7%; Score 334.5; DB 6; Length 254;
Best Local Similarity 34.1%; Pred. No. 2.2e-25;
Matches 92; Conservative 54; Mismatches 87; Indels 37; Gaps 9;

QY 28 GVLLVGLLLNSLALWVFCRMOQMTETRIYMTNLAVADLCCLCTL-PFVLHSLRD---T 83
   |||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 1 GNLLVILVILRTKCL-----RTPTNIFLNLAVALDILLFLLTPPWALYLVGGDW 51

QY 84 SDTPLCQLSQGIYLTNRYSISLVTAIVDRYVAVRHPLRARGLSRPRQAAAVCAVLWL 143
   |||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 52 FGDALCKLVGALFVNGYASILLTISIDRYLAIVHPLRYRIRTPRAKVLILLVWL 111

QY 144 V-----IGSLVARMLLGIQEGG-----FCFRSTRHNFNSMRPPLLGFLYPLAVVVFCSL 192
   |||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 112 ALLSLPPLFLSWLRTVEGNTTCLIDFPESVKRSY-VLLSTLVGFVPLLVILVCYT 170

QY 193 KVVTAQAQRPPTDVG---QAEATRKAAARMVWNLVVFVCFPLHVLGTVRLAVGNACA 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 171 RILRTLKRARSQSLKRSSSRKAOKMLLVVVVFLCWLPHYHIVLL-----DSL 224

QY 250 LLETIR---RALYITSKLSDANCLDAICY 276
   |||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 225 LLSIWRVLPALLITLWLYVNSCLNPIY 254

RESULT 2
US-10-055-877-327
; Sequence 327, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muraidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Szytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Cahterine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
```

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; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 327
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 7tm_1, 7
; OTHER INFORMATION: transmembrane receptor domain consensus sequence
US-10-055-877-327

Query Match      20.7%; Score 334.5; DB 6; Length 254;
Best Local Similarity 34.1%; Pred. No. 2.2e-25;
Matches 92; Conservative 54; Mismatches 87; Indels 37; Gaps 9;

QY 28 GVLLVGLLLNSLALWVFCRMOQMTETRIYMTNLAVADLCCLCTL-PFVLHSLRD---T 83
   |||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 1 GNLLVILVILRTKCL-----RTPTNIFLNLAVALDILLFLLTPPWALYLVGGDW 51

QY 84 SDTPLCQLSQGIYLTNRYSISLVTAIVDRYVAVRHPLRARGLSRPRQAAAVCAVLWL 143
   |||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 52 FGDALCKLVGALFVNGYASILLTISIDRYLAIVHPLRYRIRTPRAKVLILLVWL 111

QY 144 V-----IGSLVARMLLGIQEGG-----FCFRSTRHNFNSMRPPLLGFLYPLAVVVFCSL 192
   |||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 112 ALLSLPPLFLSWLRTVEGNTTCLIDFPESVKRSY-VLLSTLVGFVPLLVILVCYT 170

QY 193 KVVTAQAQRPPTDVG---QAEATRKAAARMVWNLVVFVCFPLHVLGTVRLAVGNACA 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 171 RILRTLKRARSQSLKRSSSRKAOKMLLVVVVFLCWLPHYHIVLL-----DSL 224

QY 250 LLETIR---RALYITSKLSDANCLDAICY 276
   |||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
Db 225 LLSIWRVLPALLITLWLYVNSCLNPIY 254

RESULT 3
US-10-055-877-340
; Sequence 340, Application US/10055877
; Publication No. US20050288241A1
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US-10-877-346-83

Query Match 20.7%; Score 334.5; DB 6; Length 254;
Best Local Similarity 34.1%; Pred. No. 2.2e-25;
Matches 92; Conservative 54; Mismatches 87; Indels 37; Gaps 9;

Qy 28 GVLLVGLLNSLWVFCRCMQMTETRIYMTNLAVADICLCTL-PFVHSLRD---T 83
Db 1 GNLLVILVIRTKK-----RPTNIFLNLAVADLFLTPPWALYVLVGDMV 51

Qy 84 SDTFLQLSQGIYLTNRYMSISLVTAIVDRYVAVRHPLRARGLRSPROAAVCAVLWVL 143
Db 52 FGDALCKVGLFVNGYASILLTAISIDRYLAIVHPLRYRIRPRRAKVILLVWVL 111

Qy 144 V-----IGSLVARMLGIQEGG-----FCFRSTRNFMNRPPLGLGYPLAVVVFCSL 192
Db 112 ALLSLPPLFLSWLRTVEGNTTVCLIDFPESVGRSY-VLLSTLVGVFLPILVILVCYT 170

Qy 193 KVTALAQRPPTDVG---QAEATKAAVMWVWVVCFLPHVGLTVRLAVGNACA 249
Db 171 RLRLTLRKARSQSLKRRSSSRKAAMLLVVVVVFLVCWLPYHIVLLI-----DSL 224

Qy 250 LLETIR---RALYITSKLSANCLDAICY 276
Db 225 LLSIWRVLPALITLWLVNCLNPIY 254

RESULT 5

US-11-157-930-2
; Sequence 2, Application US/11157930
; Publication No. US20050266482A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/11/157,930
; PRIOR FILING DATE: 2005-06-22
; PRIOR APPLICATION NUMBER: US/09/828,478
; PRIOR FILING DATE: 2001-04-09
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-157-930-2

Query Match 19.7%; Score 317.5; DB 7; Length 346;
Best Local Similarity 28.4%; Pred. No. 1.4e-23;
Matches 89; Conservative 64; Mismatches 139; Indels 21; Gaps 10;

Qy 2 NGTYTCSSDLTPWPAIKGFY--AYLGVLVGLLNSLWVFCRCMQMTETRIYM 59
Db 20 NGTFNNNSRNC-IENFKREFPIVYL-IFFGVGLNGLSIVVFLQPYKSTSVNFM 77

Qy 60 TNLAVADICLCTLPP-VLHSLRDTs-----DTPLCQLSQGIYLTNRYMSISLVTAIVDR 114
Db 78 LNLAISDLLPSTLPPRADYLRGNSWIFGDLACRIMSLSLYV-NMYSIYFLTVLSVR 136

Qy 115 YVAVRHPLRARGLRSPROAAVCAVLWVVGSIVARMLGIQEGG---FCFRSTRNFM 171
Db 137 FLAWHPEFLRLHVTIRSAWILCOIILWILMASIMLLDSGSGVTSCLNLYKIA 196

Qy 172 SMRPP-----LLGFLYPLAVVVFCSLKVVTALAQRPPTDVQAEATKAAVMWVWV 226
Db 197 KLQTMNYIALVVGCLLPFFTLISCYLLIRVLLKVEPESGLRVSHRKALTTIITLIIF 256

Qy 227 VVCFPLPHVGLTVRLAVGNACALLETIRALYITSKLSANCLDAICYMKEPQE- 285

Db 257 FLCFLPYHTLRTVHLTT-WKVGCLCKDRHLKALVITLALAAANACFNPLLYFAGENFKDR 315
Qy 286 -ASALAVAPRAKA 297
Db 316 LKSALRKGHPOKA 328

RESULT 6
US-10-995-561-545
; Sequence 545, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 545
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-545

Query Match 19.5%; Score 315.5; DB 6; Length 365;
Best Local Similarity 29.1%; Pred. No. 2.3e-23;
Matches 93; Conservative 55; Mismatches 127; Indels 45; Gaps 11;

Qy 29 VLLVGLLNSLWVFCRCMQMTETRIYMTNLAVADICLCTLPLVHSLRDTSDTP- 87
Db 44 VVFLVGLGLNAPTLMFLPRLPMDATATYMFHLASDTLYVLSLPTLIYYAAHNHWP 103

Qy 88 ---LQQLSQGIYLTNRYMSISLVTAIVDRYVAVRHPLRARGLRSPROAAVCAVLWVL 144
Db 104 GTEICKVPRFLPYMNLGYSLVFLTCISVHYRIGIICPLRALWGRPLAGLCLAVLVV 163

Qy 145 IGSILVAR-WLLGIQEGG---FCFRSTR-----H--NFNSMRPFLGLFYPLAVVVFCSLK 193
Db 164 AGCLVPLNFPVTTNKGTTVLCHDITRPEFDHYVHFSSAVMGLL-FGVPCLVTLVCYL 222

Qy 194 VVTALAQRPPTDVQAEATKAAVMWVWVWVVCFLPLHVLGLTV-----RLAVGNACA 249
Db 223 MARRLYQ-PLPGSAQSSSLRSLRTIAVVLTVFAVCFVPFHITRTIYLLARLEA--DCR 279

Qy 250 LLETIRALYITSKLSANCLDAICYMKEPQE-----ASALAVAP 293
Db 280 VLNIVNVVYKVTPLASANSCLDPVLYLLTGDKYRRLQRLCGCGGKQPRTAASSLAVS 339

Qy 294 RAK-----AHKSQDSLCTV 307
Db 340 LPEDSSCRWAATPQDSSCST 359

RESULT 7

US-11-127-877-52
; Sequence 52, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merckhiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. P.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12

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; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-52

Query Match      19.4%; Score 312.5; DB 7; Length 391;
Best Local Similarity 27.6%; Pred. NO. 4.9e-23;
Matches 89; Conservative 54; Mismatches 128; Indels 51; Gaps 9;

Qy 1 MNGYNTCGSDLTW-----PPAIVLGFYAVIGLVLTGLLNSLALWVFCRQW 52
Db 38 LMGTFASQKCPQVEMGLWNTIQPP-----FLWLVFLVATLENIFVLSVFCVHKS 89

Qy 53 TETRIYMTNLAVADLCCLCTLPFVLHSLRDTSD-----TPLCQLSQGIYLTNRYMSISLVT 108
Db 90 TVAEIYGLNLAADULLACGLPFWAITISNPNFDMFLGFTLCRVVNAIISMNLYSSICFLM 149

Qy 109 AIAVDYVAVRHLRARGLSRQAAVCAVLW--VLVIGS--LVARWLLGIQEGGFCFR 164
Db 150 LVSIDRYLALVKTSMGRMGRVWAKYLSLVINGCTLLSSPMLVFTMTKEYSDEG---- 205

Qy 165 STRYN-----FNSMRPFLGVLPLAVVFCSLKVVVTALAQRPPTDVQQA 209
Db 206 ---HNVTACVISYPSLIWEVFTNMLNVGVFLPLSVITFTCTMQIMQVLRNEMQKFKEI 262

Qy 210 EATKKAARMVWANTLVFVCFPLHVGTV---RLAVGWACALLETIRRALYITSKLS 265
Db 263 QTERATVILVLLVLLFFIICMLDPPFOISTFDLHLRLGI--LSSCQDERIIDVITQIASFWA 321

Qy 266 DANCCDAICYYYMAKBFQEAS 287
Db 322 YSNSCLNPLVYVIVGKRFKKS 343

RESULT 8
US-10-055-877-225
; Sequence 225; Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Cahterine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference

; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 225
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 7tm_1 domain
; OTHER INFORMATION: consensus sequence
US-10-055-877-225

Query Match      18.9%; Score 305; DB 6; Length 259;
Best Local Similarity 33.0%; Pred. NO. 1.6e-22;
Matches 93; Conservative 49; Mismatches 84; Indels 56; Gaps 10;

Qy 28 GVLLVGLLLNSLALWVFCRQWQWETRIYMTNLAVADLCCLCTLPFVLHSLRDTSD- 85
Db 1 GNLLVILVILRTKGL-----RTPNIFILNLAVADLFLFLTLPLPWALYLVGGSD 51

Qy 86 ----TPLCQLSQGIYLTNRYMSISLVTAVDVYVAVRHLRARGLR--SPRQAAVCAVL 140
Db 52 WPFSGALCVTVALDVVNNYASILLTALSIDRYLAVIHPLEYRRRTSPRAKVVILLV 111

Qy 141 WVLV----IGSLVARWLLGIQEGG-----FCFRSTRNFMNMR-----FPLL 178
Db 112 WVALLLSLPLPFSWKTVEEGNGLNVNVTVCLIDFPEBSTASVSTWLSRVLLSTLV 171

Qy 179 GFLYPLAVVFCSLKVVVTALAQRPPTDVQQAETKKAARMVWANTLVFVCFPLHVG 237
Db 172 GFLLPLLVILVCYTRILRTL-----RKAARTLLVWVWVFLVCLWLPYFVILL 217

Qy 238 --TVLAVGWNA-CALLEITIREALYITSKLSDANCCDAICY 276
Db 218 LDTLCLSIIMSSTCSELRVLPALLVTLWLVAVNSCLNPLIY 259

RESULT 9
US-10-055-877-237
; Sequence 237; Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
```

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1  APPLICANT: Gerlach, Valerie
2  APPLICANT: Spytek, Kimberly
3  APPLICANT: Ratelli, Luca
4  APPLICANT: Kekuda, Ramesh
5  APPLICANT: Guo, Xiaojia
6  APPLICANT: Zerhusen, Bryan
7  APPLICANT: Andrew, David
8  APPLICANT: Mezes, Peter
9  APPLICANT: Patturajan, Meera
10 APPLICANT: Burgess, Catherine
11 APPLICANT: Eissen, Andrew
12 APPLICANT: Wolenc, Adam
13 APPLICANT: Baumgartner, Jason
14 APPLICANT: Shimkets, Richard
15 APPLICANT: Gusev, Vladimir
16 APPLICANT: Vernet, Corine
17 APPLICANT: Taupier Jr., Raymond
18 APPLICANT: Pena, Carol
19 APPLICANT: Shenoy, Suresh
20 APPLICANT: Li, Li
21 APPLICANT: Casman, Stacie
22 APPLICANT: Boldog, Ference
23
24 TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
25
26 FILE REFERENCE: 21402-251
27
28 CURRENT APPLICATION NUMBER: US/10/055,877
29
30 CURRENT FILING DATE: 2002-01-22
31
32 PRIOR APPLICATION NUMBER: 60/262,892
33
34 PRIOR FILING DATE: 2001-01-19
35
36 PRIOR APPLICATION NUMBER: 60/263,598
37
38 PRIOR FILING DATE: 2001-01-23
39
40 PRIOR APPLICATION NUMBER: 60/263,799
41
42 PRIOR FILING DATE: 2001-01-24
43
44 PRIOR APPLICATION NUMBER: 60/264,117
45
46 PRIOR FILING DATE: 2001-01-25
47
48 PRIOR APPLICATION NUMBER: 60/264,139
49
50 PRIOR FILING DATE: 2001-01-25
51
52 PRIOR APPLICATION NUMBER: 60/264,478
53
54 PRIOR FILING DATE: 2001-01-26
55
56 PRIOR APPLICATION NUMBER: 60/263,351
57
58 PRIOR FILING DATE: 2001-01-30
59
60 PRIOR APPLICATION NUMBER: 60/272,870
61
62 PRIOR FILING DATE: 2001-03-02
63
64 PRIOR APPLICATION NUMBER: 60/275,990
65
66 PRIOR FILING DATE: 2001-03-14
67
68 PRIOR APPLICATION NUMBER: 60/275,927
69
70 PRIOR FILING DATE: 2001-03-14
71
72 REMAINING Prior Application data removed - See File Wrapper or PALM.
73
74 NUMBER OF SEQ ID NOS: 512
75
76 SOFTWARE: PatentIn Ver. 2.1
77
78 SEQ ID NO 237
79
80 LENGTH: 259
81
82 TYPE: PRT
83
84 ORGANISM: Artificial Sequence
85
86 FEATURE:
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88 OTHER INFORMATION: Description of Artificial Sequence: 7cm_1 domain
89
90 OTHER INFORMATION: consensus sequence
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Query Match	18.9%	Score 305;	DB 6;	Length 259;
Best Local Similarity	33.0%	Pred. No. 1.6e-22;		
Matches 93; Conservative 49; Mismatches 84; Indels 56; Gaps 10;				
Qy	28	GVLIVLGLLNSLALWVFCRCMQQWTRIVMTNLAVADLCLLCTL-PFVLHSLRDYSD-	85	
Db	1	GNLLVILVILTKKL-----RTPTNIFILNLAVADLLFLTLPPWALYLVGGSD	51	
Qy	86	-----TPLCOLSQGIYLTNRYMSISLVTAIAVDREVAVRHPIRLARGLR-SPRQAAAVCAVL	140	
Db	52	WPGSALCKLVATDLDVNVMYASILLTLTAISIDRYLAIVHPIRYERRRSTSPRAKVILLV	111	
Qy	141	WVLV-----IGSLVARWLLGTOEG-----FCFSTRTHNFNSMR-----FPLL	178	
Db	112	WVLALLSLPLFLFSWTKVTEEGNGTLNVNVTCVLDIPPESTASVSTWLRSYVLLSTLV	171	

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QY 179 GFYIPLAVVFCSLKVVTLAQRPTDVQGAERTKAARMWVANLLVFVFCPLHVL- 2377
    |||||:::||||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 172 GFLPFLLLVILVCYTRILETL-----RKAARTLLVVVVVFCWLPYFVILL 217
    |||||:::||||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 238 --TVRLAVGWNA-CALLETRIRALYITSKLSANCLDAICY 276
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Db 218 LDTLCLSITMSTCELEERVLPTALLVTIWLAYVNSCLNPIY 259
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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RESULT 10
US-11-157-930-4
; Sequence 4, Application US/11157930
; Publication No. US20050256482A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yongchang
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; TITLE OF INVENTION: Protein
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/11/157,930
; CURRENT FILING DATE: 2005-06-22
; PRIOR APPLICATION NUMBER: US/09/828,478
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 339

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; TYPE: PRT
; ORGANISM: Homo sapiens

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ORGANISM: H
US-11-157-930-4

Query Match	18.6%;	Score 300;	DB 7;	Length 339;
Best Local Similarity	29.1%;	Pred. No. 6.8e-22;		
Matches 88;	Conservative 54;	Mismatches 128;	Indels 32;	Gaps 8

[illegible]

RESULT 11
US-11-157-930-6
; Sequence 6, Application US/11157930
; Publication No. US20050266482A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; TITLE OF INVENTION: protein
; FILE REFERENCES: 04974.00458

```
; CURRENT APPLICATION NUMBER: US/11/157,930
; CURRENT FILING DATE: 2005-06-22
; PRIOR APPLICATION NUMBER: US/09/828,478
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-157-930-6

Query Match      18.6%; Score 300; DB 7; Length 367;
Best Local Similarity 29.1%; Pred. No. 7.4e-22;
Matches 88; Conservative 54; Mismatches 128; Indels 32; Gaps 8;

Qy  4 TYNTCGSSDLTWPAPKLGFYAYLGLVLLGLLNSLALWVFCRMOQWETRIYMTNLA 63
Db  47 TAEQCGQE---TLENMLFASFYLLDFILALVGNLTALWLFIRDHKSGETPANVFLMHLA 102
Qy  64 VADLCCLCTLPVHLSLRDTSDTPL---COLSQGIYLTNNYMSISLVTALADRYAVR 119
Db  103 VADLSCVLVLTPLVYHSGHNWPFGEIACRLTGFLFVLYNMYASIFYLTCSADRFLAIV 162
Qy  120 HPLRARGLSRQAAAVCAVLWLVIGS---LVARWLGLTQEGFCF---RSTRNRP 170
Db  163 HPVRSKLRRPLYAHLACAFVWVAVAPLNVSPQVTQNTHTVVCILYREKASHAL 222
Qy  171 NSMRPPLGLFVPLAVVVFCSLKVVTALAQRPPTDVG---QAEATRKAAWVWVWV 227
Db  223 VSL---AVATFPPTTTCVLLIIRSLQ-----GLRVEKRLTKAVRMIAIVLAIPL 273
Qy  228 VCFPLHVLGLTV---RLAVGNACALLETIRRALYITSKLSANCLDAICYVYMAKEFQ 284
Db  274 VCFVPHVNRVYVLYHRSHGASCATORILALANRITSCLISLNGALDPIMYFFVABEKR 333
Qy  285 EA 286
Db  334 HA 335

RESULT 12
US-11-127-877-46
; Sequence 46, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 46
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-46

Query Match      18.5%; Score 298.5; DB 7; Length 373;
Best Local Similarity 26.2%; Pred. No. 1.1e-21;
Matches 88; Conservative 54; Mismatches 128; Indels 32; Gaps 8;

Qy  1 MNGTYNTCGSSDLTWPAPKLGFYAYLGLVLLGLLNSLALWVFCRMOQWETRIYMT 60
Db  45 LHGTF-----PGLCVMAVHGAIFLAGLVNLGLADLYVFCRTRAKTPSVIYTI 93
Qy  61 NLAVADL-----CLLCTLPFVHLSLRDTSDTPLCQLSQGIYLTNNYMT 102
Db  94 NLVWTDLLVGLSLPTRFVYVYGCARGLRCAPFHVLG-----YFLNMHC 136
Qy  103 SISLVTALADRYAVRHLPLRARGLSRQAAAVCAVLWLVIGSLVARWLGLIQEGFCF 162
Db  137 SILFLTCICVDRLAIVRPEAPACQACARAVCAFMV-LAAGA-VTLVSLVGLVTSRPC 194
Qy  163 FRSTRHNFNSMRPPLGLFVPLAVVVFCSLKVVTALAQRPPTDVGQAEATR-KAARMVWA 221
Db  195 CR-----VFALTVLEFLPLLVISVFTGRINCALSRR-PGLLHGRRORRRVAMQLLIT 245

Matches 88; Conservative 72; Mismatches 137; Indels 39; Gaps 10;

Qy  3 GTYNTCGSSDLTWPAPKLGFYAYLGLVLLGLLNSLALWVFCR 48
Db  20 GPGSSNGNSTVASTAAVSSSFKCACTKTGFQFYVLPVAVILVFTIGLNSVAIMFVFFH 79
Qy  49 MQQWETRIYMTNLAADLCLCTLPVHLSLRDTSD---TPLCQLSQGIYLTNNYMSI 104
Db  80 MKPWSGISVTMNFNLADFLYVLTLPALIFYFNKNTDMIFGDAMCKLQRFHFHVNLYGSI 139
Qy  105 SLVTAIAVDRYAVRHLPLRARGLSRQAAAVCAVLWLV---IGSLVARWLGLIOEGG- 160
Db  140 LFTCTISAHRYSGVVIYELKSLGRKKNAICISVLWVLIIVVAISPILFYSGTGVRKNKT 199
Qy  161 -FCFRSTRNRP-----NSMRPPLGLFVPLAVVVFCSLKVVTALAQRPPTDVGQAEATR 213
Db  200 ITCYDVTTSDEYLSRYFYISNCTTVAMFCVPLVLLGCVGLIVRALIYK---DLONSPLRR 256
Qy  214 KAARMVWVWVWVVFVFCFLPHVGLTVRLAVGNW-----ACALLETIRRALYITSKLSAN 268
Db  257 KSIYLVIIIVLTVFAVSYPFHVMTNLRARLDFQTPAMCAFNDRVVATYQVTRGLASLN 316
Qy  269 CCLDAICYVYMAKEFQAEASALAVAPRAKAKHSQDSL 304
Db  317 SCVDPIDYFLAGDTFRR--RLSRATRKASRRSEANL 350

RESULT 13
US-11-127-877-66
; Sequence 66, Application US/11/127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 66
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-66

Query Match      18.4%; Score 297.5; DB 7; Length 358;
Best Local Similarity 29.4%; Pred. No. 1.3e-21;
Matches 89; Conservative 42; Mismatches 111; Indels 61; Gaps 9;

Qy  1 MNGTYNTCGSSDLTWPAPKLGFYAYLGLVLLGLLNSLALWVFCRMOQWETRIYMT 60
Db  45 LHGTF-----PGLCVMAVHGAIFLAGLVNLGLADLYVFCRTRAKTPSVIYTI 93
Qy  61 NLAVADL-----CLLCTLPFVHLSLRDTSDTPLCQLSQGIYLTNNYMT 102
Db  94 NLVWTDLLVGLSLPTRFVYVYGCARGLRCAPFHVLG-----YFLNMHC 136
Qy  103 SISLVTALADRYAVRHLPLRARGLSRQAAAVCAVLWLVIGSLVARWLGLIQEGFCF 162
Db  137 SILFLTCICVDRLAIVRPEAPACQACARAVCAFMV-LAAGA-VTLVSLVGLVTSRPC 194
Qy  163 FRSTRHNFNSMRPPLGLFVPLAVVVFCSLKVVTALAQRPPTDVGQAEATR-KAARMVWA 221
Db  195 CR-----VFALTVLEFLPLLVISVFTGRINCALSRR-PGLLHGRRORRRVAMQLLIT 245
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QY 222 NLAVFVVCFLPLHVLTVRLAVGWNACALLETTIRRALYITSKLSDANCLDAICYVMK 281
Db 246 VLIIFLCVCFPPFRAR----QVAVALWPMHPHTSLVVYHVAUTLSLNSCMDPIVCFVTS 302
QY 282 EFQ 284
Db 303 GFQ 305

RESULT 14
US-10-995-561-523
; Sequence 523, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 523
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-523

Query Match 17.9%; Score 288.5; DB 6; Length 352;
Best Local Similarity 26.2%; Pred. No. 9.2e-21;
Matches 75; Conservative 62; Mismatches 118; Indels 31; Gaps 8;

QY 16 PPAIKLGP-YAYLGVLLVGLLNSLALWVFCRMOQWETRIYMTNLAVADICLLCTLP 74
Db 34 PPLYSLVFIFGFGVGNMLVILIN-----CKRLKSMTD--IYLLNLAISDLFFLLTVP 84
QY 75 FVLHSLRDTSD--TPLCQLSQGIYLTNRNYSISLVTATAVDRYAVVRHPLRAGLSRPQ 132
Db 85 FWAHAAAQWDFGNTMCQLTGLYFIFGFGIFILLTIDRYLAVVHAFALKARTVTF 144
QY 133 AAACAVLWVL-VIGSLVARWLLGIQGGFCFPRSTRH-----NFNSMRFPPLLGFY 181
Db 145 GVTVSVITWVAVFASLPGIIFTRSQEGHLYTCSSHPFYSQYQFWMNFOTLKIVILGLV 204
QY 182 LPLAVVFCSLKVVTALAQRPPTDVGOAEATRKAAARMVWNLVVFVVCFLPHVGL---T 238
Db 205 LPLLVMVICYSIGILKTLR-----CRNEKKRRAVRLIFTIMIVYFLWAPYNIIVLLNT 259
QY 239 VRLAVGWNACALLETTIRRALYITSKLSDANCLDAICYVMK 284
Db 260 PQBFPGNLNCSNRLDQAMQVETLGMTHCCINPIIYAFVGEKPR 305

RESULT 15
US-11-068-686-2
; Sequence 2, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; ; Schweickart, Vicki L.
; ; Report, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/068,686
FILING DATE: 28-Feb-2005
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: /= "88C amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-11-068-686-2

Query Match 17.9%; Score 288.5; DB 7; Length 352;
Best Local Similarity 26.2%; Pred. No. 9.2e-21;
Matches 75; Conservative 62; Mismatches 118; Indels 31; Gaps 8;

QY 16 PPAIKLGP-YAYLGVLLVGLLNSLALWVFCRMOQWETRIYMTNLAVADICLLCTLP 74
Db 34 PPLYSLVFIFGFGVGNMLVILIN-----CKRLKSMTD--IYLLNLAISDLFFLLTVP 84
QY 75 FVLHSLRDTSD--TPLCQLSQGIYLTNRNYSISLVTATAVDRYAVVRHPLRAGLSRPQ 132
Db 85 FWAHAAAQWDFGNTMCQLTGLYFIFGFGIFILLTIDRYLAVVHAFALKARTVTF 144
QY 133 AAACAVLWVL-VIGSLVARWLLGIQGGFCFPRSTRH-----NFNSMRFPPLLGFY 181
Db 145 GVTVSVITWVAVFASLPGIIFTRSQEGHLYTCSSHPFYSQYQFWMNFOTLKIVILGLV 204
QY 182 LPLAVVFCSLKVVTALAQRPPTDVGOAEATRKAAARMVWNLVVFVVCFLPHVGL---T 238
Db 205 LPLLVMVICYSIGILKTLR-----CRNEKKRRAVRLIFTIMIVYFLWAPYNIIVLLNT 259
QY 239 VRLAVGWNACALLETTIRRALYITSKLSDANCLDAICYVMK 284
Db 260 PQBFPGNLNCSNRLDQAMQVETLGMTHCCINPIIYAFVGEKPR 305

Search completed: February 9, 2006, 01:21:41
Job time : 11.5 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 00:47:43 ; Search time 165 Seconds

(without alignments)
1321.262 Million cell updates/sec

Title: US-10-083-168-16

Perfect score: 1614

Sequence: 1 MNGTYNTCGSSDLTWPPAIK.....AVAPRAKHSQDSILCVTLA 309

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1608	99.6	309	Q6FH18_HUMAN	Q6fh18 homo sapien
2	1602	99.3	309	Q4SPQ4_TETNG	Q4spq4 tetraodon n
3	1602	99.3	309	Q4SPQ4_TETNG	Q4spq4 tetraodon n
4	1602	99.3	309	Q4SPQ4_TETNG	Q4spq4 tetraodon n
5	1597	98.9	308	Q4VBN1_HUMAN	Q4vbn1 homo sapien
6	1124	69.6	307	Q4VBN1_HUMAN	Q4vbn1 homo sapien
7	1124	69.6	307	Q4VBN1_HUMAN	Q4vbn1 homo sapien
8	1123	69.6	307	Q4VBN1_HUMAN	Q4vbn1 homo sapien
9	1109	68.7	307	Q4VBN1_HUMAN	Q4vbn1 homo sapien
10	417.5	25.9	305	Q4TAH0_TETNG	Q4tah0 tetraodon n
11	403	25.0	370	Q502U9_HUMAN	Q502u9 homo sapien
12	402	24.9	370	Q502U9_HUMAN	Q502u9 homo sapien
13	400	24.8	370	Q502U9_HUMAN	Q502u9 homo sapien
14	400	24.8	370	Q502U9_HUMAN	Q502u9 homo sapien
15	392	24.3	370	Q8BLG2_MOUSE	Q8blg2 mus musculus
16	376.5	23.3	302	Q4S8W3_TETNG	Q4s8w3 tetraodon n
17	376	23.3	319	Q4S8W3_TETNG	Q4s8w3 tetraodon n
18	375.5	23.3	363	Q8TDS4_HUMAN	Q8tds4 homo sapien
19	368.5	22.8	308	Q4RFP7_TETNG	Q4rfp7 tetraodon n
20	368.5	22.8	387	Q4RFP7_TETNG	Q4rfp7 tetraodon n
21	368.5	22.8	387	Q4RFP7_TETNG	Q4rfp7 tetraodon n
22	368	22.8	347	Q7ZZA4_BRARE	Q7zza4 brachydanio
23	365.5	22.6	296	Q9WU09_RAT	Q9wu09 rattus norv
24	365	22.6	345	Q4RFP7_TETNG	Q4rfp7 tetraodon n
25	362	22.4	372	Q5KU18_HUMAN	Q5ku18 homo sapien
26	362	22.4	372	Q5KU18_HUMAN	Q5ku18 homo sapien
27	361.5	22.4	344	Q4RFP7_TETNG	Q4rfp7 tetraodon n
28	357.5	22.1	344	Q4RFP7_TETNG	Q4rfp7 tetraodon n
29	356	22.1	344	Q4G072_RAT	Q4g072 rattus norv
30	355.5	22.0	344	Q53FA0_HUMAN	Q53fa0 homo sapien
31	348.5	21.6	360	Q9EP66_MOUSE	Q9ep66 mus musculus

32 343 21.3 358 2 Q4SPQ4_TETNG Q4spq4 tetraodon n
33 338.5 21.0 360 2 Q80Z39_RAT Q80z39 rattus norv
34 331.5 20.5 374 1 P2RY2_RAT P2ry2 rattus norv
35 331 20.5 298 2 Q8VE54_MOUSE Q8ve54 mus musculus
36 330.5 20.5 377 1 P2RY2_HUMAN P2ry2 homo sapien
37 328 20.3 345 2 Q4VBN1_HUMAN Q4vbn1 homo sapien
38 327 20.3 323 2 Q5XGS6_XENLA Q5xgs6 xenopus lae
39 327 20.3 346 1 GPR81_HUMAN Gpr81 homo sapien
40 322.5 20.0 345 1 CLTR2_PIG Cltr2 sus scrofa
41 321 19.9 349 2 Q6P852_XENTR Q6p852 xenopus tro
42 320.5 19.9 343 1 GPR81_MOUSE Gpr81 mus musculus
43 320.5 19.9 361 1 P2RY4_RAT P2ry4 rattus norv
44 319.5 19.8 373 2 Q5YA25_PIG Q5ya25 sus scrofa
45 319 19.8 328 1 P2RY6_RAT P2ry6 rattus norv

ALIGNMENTS

RESULT 1

ID Q6FH18_HUMAN PRELIMINARY; PRT; 309 AA.
AC Q6FH18;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE GPR35 protein.
GN Name=GPR35;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Katrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; CR541765; CAG46564.1; -; mRNA.
DR GO; GO:001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 309 AA; 34141 MW; FC034FB7231B26F1 CRC64;

Query Match 99.6%; Score 1608; DB 2; Length 309;
Best Local Similarity 99.7%; Pred. No. 1.7e-112;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFYALGVLVGLLNLALWVFCRCMQQTETRIYMT 60
|||||
Db 1 MNGTYNTCGSSDLTWPPAIKLGFYALGVLVGLLNLALWVFCRCMQQTETRIYMT 60
61 NLAVADLCCLCTLPVHLHSLRDTSDPLCQLSGIYLTNRYMSISLVTAIVDYYAVVRH 120
61 NLAVADLCCLCTLPVHLHSLRDTSDPLCQLSGIYLTNRYMSISLVTAIVDYYAVVRH 120
121 PLRARGLRSPROAAAVCAVLVWLVIGSLVARMLLGIQEGGFCFRTRHNFNSRPLLG 180
121 PLRARGLRSPROAAAVCAVLVWLVIGSLVARMLLGIQEGGFCFRTRHNFNSRPLLG 180
181 YLPVAVVFCSLKVVTALAQRPPTDVQAEATKAAKRWANLLVTVVFCPLPLVGLTVR 240
181 YLPVAVVFCSLKVVTALAQRPPTDVQAEATKAAKRWANLLVTVVFCPLPLVGLTVR 240

QY	241	LAVGNACALLETTIRALYITTSKLSANDCCCLDAICYTMAKEFQASALAVAPRAKAKS	300
Db	241	LAVGNACALLETTIRALYITTSKLSANDCCCLDAICYTMAKEFQASALAVAPRAKAKS	300
QY	301	QDSLCVTLA 309	
Db	301	QDSLCVTLA 309	
RESULT 2			
GPR35 HUMAN			
ID	GPR35 HUMAN	STANDARD; PRT; 309 AA.	
AC	Q9HC97; Q43495; Q8CUH4;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	13-SEP-2005 (Rel. 48, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DE	Probable G-protein coupled receptor 35.		
GN	Names=GPR35;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE, AND VARIANT ARG-294.		
RX	MEDLINE=98140132; PubMed=9479503; DOI=10.1006/geno.1998.5095;		
RA	O'Dowd B.F., Nguyen T., Marchese A., Cheng R., Lynch K.R.,		
RA	Heng H.H.Q., Kolakowski L.F. Jr., George S.R.;		
RT	"Discovery of three novel G-protein-coupled receptor genes.";		
RL	Genomics 47:310-313 (1998).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE, AND VARIANTS THR-25; ILE-29; MET-108; SER-125 AND		
RP	MET-253.		
RX	MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;		
RA	Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,		
RA	Hinokio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,		
RA	del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla S.,		
RA	Polsensky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,		
RA	Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,		
RA	Bell G.I.;		
RT	"Genetic variation in the gene encoding calpain-10 is associated with		
RT	type 2 diabetes mellitus.";		
RL	Nat. Genet. 26:163-175 (2000).		
RN	[3]		
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].		
RA	Warren C.N., Aronstam R.S., Sharma S.V.;		
RT	"cDNA clones of human proteins involved in signal transduction		
RT	sequenced by the Guthrie cDNA resource center (www.cdna.org).";		
RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: Orphan receptor.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).		
CC	-1- TISSUE SPECIFICITY: Expressed in all adult and fetal tissues		
CC	examined, including pancreatic islets and skeletal muscle, with		
CC	relatively higher levels in adult lung, small intestine, colon and		
CC	stomach.		
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.		
CC	-----		
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use as long as its content is in no way modified and this statement is not		
CC	removed.		
CC	-----		
DR	EMBL; AF027957; AAC52028.1; -; Genomic_DNA.		
DR	EMBL; AF089087; AG17965.1; -; mRNA.		
DR	EMBL; AY275467; AAP32299.1; -; Genomic_DNA.		
DR	Ensembl; ENSG00000178623; Homo sapiens.		
DR	HGNC; HGNC:4492; GPR35.		
DR	MIM; 602646; -.		
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.		
DR	GO; GO:0004930; F:G-protein coupled receptor activity; TAS.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.		
DR	InterPro; IPR000276; GPCR_Rhodopsin.		
DR	PRINTS; PRO0237; GPCRHOOPS.		
DR	PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.		
DR	PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.		
KW	G-protein coupled receptor; Glycoprotein; Polymorphism; Receptor;		
KW	Transducer; Transmembrane.		
FT	TOPO_DOM 1 24 Extracellular (Potential).		
FT	TRANSMEM 25 45 1 (Potential).		
FT	TOPO_DOM 46 56 Cytoplasmic (Potential).		
FT	TRANSMEM 57 77 2 (Potential).		
FT	TOPO_DOM 78 90 Extracellular (Potential).		
FT	TRANSMEM 91 112 3 (Potential).		
FT	TOPO_DOM 113 135 Cytoplasmic (Potential).		
FT	TRANSMEM 136 156 4 (Potential).		
FT	TOPO_DOM 157 174 Extracellular (Potential).		
FT	TRANSMEM 175 195 5 (Potential).		
FT	TOPO_DOM 196 218 Cytoplasmic (Potential).		
FT	TRANSMEM 219 239 6 (Potential).		
FT	TOPO_DOM 240 258 Extracellular (Potential).		
FT	TRANSMEM 259 279 7 (Potential).		
FT	TOPO_DOM 280 309 Cytoplasmic (Potential).		
FT	CARBOHYD 2 2 N-linked (GlcNAc. . .) (Potential).		
FT	DISULFID 89 162 BY similarity.		
FT	VARIANT 25 25 A -> T.		
FT	VARIANT 29 29 /FTID=VAR_013601.		
FT	VARIANT 108 108 V -> I.		
FT	VARIANT 125 125 /FTID=VAR_013602.		
FT	VARIANT 253 253 T -> M.		
FT	VARIANT 294 294 /FTID=VAR_013603.		
FT	VARIANT 174 174 R -> S.		
FT	CONFLICT 174 174 A -> R (in Ref. 1).		
SQ	SEQUENCE 309 AA; 34072 MW; 97734FB7231B26F0 CRC64;		
Query Match 99.3%; Score 1602; DB 1; Length 309;			
Best Local Similarity 99.4%; Pred. No. 4.9e-112;			
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	1	MNGTYNTCGSSDLTWPPAIKLGFYALGVLVGLVGLLNSLALWVFCRMOQTETRIYMT	60
Db	1	MNGTYNTCGSSDLTWPPAIKLGFYALGVLVGLVGLLNSLALWVFCRMOQTETRIYMT	60
QY	61	NLAVALDCLLCTLPFLVLSRLTSDTPLCQLSQGIYLTNRYMSISLVTAIVDRAVVRH	120
Db	61	NLAVALDCLLCTLPFLVLSRLTSDTPLCQLSQGIYLTNRYMSISLVTAIVDRAVVRH	120
QY	121	PLRARGLSRQAAAVCAVLAQRPTDVGAETKAAKRMVWNLVVFVCFPLHVLTVR	240
Db	121	PLRARGLSRQAAAVCAVLAQRPTDVGAETKAAKRMVWNLVVFVCFPLHVLTVR	240
QY	181	YUPLAVVVFCSLKVTALAQRPTDVGAETKAAKRMVWNLVVFVCFPLHVLTVR	240
Db	181	YUPLAVVVFCSLKVTALAQRPTDVGAETKAAKRMVWNLVVFVCFPLHVLTVR	240
QY	241	LAAGNACALLETTIRALYITTSKLSANDCCCLDAICYTMAKEFQASALAVAPRAKAKS	300
Db	241	LAAGNACALLETTIRALYITTSKLSANDCCCLDAICYTMAKEFQASALAVAPRAKAKS	300
QY	301	QDSLCVTLA 309	
Db	301	QDSLCVTLA 309	
RESULT 3			
Q4ZPV2 HUMAN			
ID	Q4ZPV2 HUMAN	PRELIMINARY; PRT; 309 AA.	
AC	Q4ZPV2;		
DT	13-SEP-2005 (Tremblrel. 31, Created)		
DT	13-SEP-2005 (Tremblrel. 31, Last sequence update)		

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein GPR35.
 GN Name=GPR35;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Haakenson W., Trani L., Schatzkammer K.;
 RA "The sequence of Homo sapiens BAC clone RP11-27M15."
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.H.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Wilson R.K.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 DR EMBL; AC124862; AAX8945.1; -; Genomic_DNA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PS00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
 DR PROSITE; PS02662; G-PROTEIN RECF_F1_2; 1.
 KW G-protein coupled receptor; Hypothetical protein; Receptor;
 KW Transducer; Transmembrane.
 SQ SEQUENCE 309 AA; 34072 MW; 97734FB7231B26F0 CRC64;

 Query Match 99.3%; Score 1602; DB 2; Length 309;
 Best Local Similarity 99.4%; Pred. No. 4.9e-112;
 Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 1 MNGTYNTCGSSDLTPWPAIKLGFAYLVGLVLLGLLNSLALWVFCRQMQWTETRIYMT 60
 DB 1 MNGTYNTCGSSDLTPWPAIKLGFAYLVGLVLLGLLNSLALWVFCRQMQWTETRIYMT 60
 QY 61 NLAVADLCCLCTLPFVLSLRDSTPLCQLSQGIYLTNRNYSISLVTAIAVDYVAVRH 120
 DB 61 NLAVADLCCLCTLPFVLSLRDSTPLCQLSQGIYLTNRNYSISLVTAIAVDYVAVRH 120
 QY 121 PLRAGRLSPROAAVCAVLVLTGSLVARWLLGIQEGGFCFRTRHNFSMRPPLG 180
 DB 121 PLRAGRLSPROAAVCAVLVLTGSLVARWLLGIQEGGFCFRTRHNFSMRPPLG 180
 QY 181 YLPLAVVFCSLKVVTTALAQRPPTDVGOAEATRKARVMWANLLVFWVCFPLPHVGLTVR 240
 DB 181 YLPLAVVFCSLKVVTTALAQRPPTDVGOAEATRKARVMWANLLVFWVCFPLPHVGLTVR 240
 QY 241 LAVGNACALLETTIRALYITSKLSANDCCCLDAICYNNMAKEFOEASALAVAPRAKHK 300
 DB 241 LAVGNACALLETTIRALYITSKLSANDCCCLDAICYNNMAKEFOEASALAVAPRAKHK 300
 QY 301 QDSLVCVTLA 309
 DB 301 QDSLVCVTLA 309

 RESULT 4
 Q6ZMP9 HUMAN
 ID Q6ZMP9 HUMAN PRELIMINARY; PRT; 394 AA.
 AC Q6ZMP9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein FLJ16773.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
 RA Osuiki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
 RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
 RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
 RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 DR EMBL; AK131540; BADI8676.1; -; mRNA.
 DR Ensembl; ENSG00000178623; Homo sapiens.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PS00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
 DR PROSITE; PS02662; G-PROTEIN RECF_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 394 AA; 43309 MW; 1598FD44BAE4233C CRC64;

 Query Match 99.3%; Score 1602; DB 2; Length 394;
 Best Local Similarity 99.4%; Pred. No. 6e-112;
 Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 1 MNGTYNTCGSSDLTPWPAIKLGFAYLVGLVLLGLLNSLALWVFCRQMQWTETRIYMT 60
 DB 86 MNGTYNTCGSSDLTPWPAIKLGFAYLVGLVLLGLLNSLALWVFCRQMQWTETRIYMT 145
 QY 61 NLAVADLCCLCTLPFVLSLRDSTPLCQLSQGIYLTNRNYSISLVTAIAVDYVAVRH 120
 DB 146 NLAVADLCCLCTLPFVLSLRDSTPLCQLSQGIYLTNRNYSISLVTAIAVDYVAVRH 205
 QY 121 PLRAGRLSPROAAVCAVLVLTGSLVARWLLGIQEGGFCFRTRHNFSMRPPLG 180
 DB 206 PLRAGRLSPROAAVCAVLVLTGSLVARWLLGIQEGGFCFRTRHNFSMRPPLG 265
 QY 181 YLPLAVVFCSLKVVTTALAQRPPTDVGOAEATRKARVMWANLLVFWVCFPLPHVGLTVR 240
 DB 266 YLPLAVVFCSLKVVTTALAQRPPTDVGOAEATRKARVMWANLLVFWVCFPLPHVGLTVR 325
 QY 241 LAVGNACALLETTIRALYITSKLSANDCCCLDAICYNNMAKEFOEASALAVAPRAKHK 300
 DB 326 LAVGNACALLETTIRALYITSKLSANDCCCLDAICYNNMAKEFOEASALAVAPRAKHK 385
 QY 301 QDSLVCVTLA 309
 DB 386 QDSLVCVTLA 394

 RESULT 5
 QAVEN5 HUMAN
 ID QAVEN5 HUMAN PRELIMINARY; PRT; 308 AA.
 AC QAVEN5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE GPR35 protein (Fragment).
 GN Name=GPR35;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TSSUE=G-protein coupled receptors;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TSSUE=G-protein coupled receptors;
 RG NIH MGC Project;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 DR EMBL; BC095500; AAH95500.1; -; mRNA.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
 DR PROSITE; PS00262; G PROTEIN RECP F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 FT NON_TER 1
 FT NON_TER 308
 FT SEQUENCE 308 AA; 33941 MW; 5791BP9CE7206034 CRC64;
 Query Match 98.9%; Score 1597; DB 2; Length 308;
 Best Local Similarity 99.4%; Pred. No. 1.le-111;
 Matches 306; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 NGTYNTCGSDLTWPPAIGKGFAYILGVLLVGLLNSLALWVFCRMOQWETRIYMTN 61
 DB 1 NGTYNTCGSDLTWPPAIGKGFAYILGVLLVGLLNSLALWVFCRMOQWETRIYMTN 60
 QY 62 LAVADICLLCTLPFLVLSLRDTSPTLQCSQGLYLTNRVMSISLVATAVDVRYAVRHP 121
 DB 61 LAVADICLLCTLPFLVLSLRDTSPTLQCSQGLYLTNRVMSISLVATAVDVRYAVRHP 120
 QY 122 LRARGLSRPRQAAAVCAVLVWLVIGSLVARWLLGIEGGFCFSTRHFNFSMFPLILGFY 181
 DB 121 LRARGLSRPRQAAAVCAVLVWLVIGSLVARWLLGIEGGFCFSTRHFNFSMFPLILGFY 180
 QY 182 LPLAVVVFCSLKVTALAPPTDVGQAEATRIKAAARMVWNLVVFVVCFLPLHVGILTVRL 241
 DB 181 LPLAVVVFCSLKVTALAPPTDVGQAEATRIKAAARMVWNLVVFVVCFLPLHVGILTVRL 240
 QY 242 AVGNACALLETIRRALYITSLKSDANCCLDAICYYTMAKBFQESALAVAPSAKHSQ 301
 DB 241 AVGNACALLETIRRALYITSLKSDANCCLDAICYYTMAKBFQESALAVAPSAKHSQ 300
 QY 302 DSLCVTLA 309
 DB 301 DSLCVTLA 308

RESULT 6
 GPR35_MOUSE
 ID GPR35_MOUSE STANDARD; PRT; 307 AA.
 AC Q9ES90;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Probable G-protein coupled receptor 35.
 GN NamesGpr35;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;
 RA Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,
 RA Hinochio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,
 RA del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla S.,
 RA Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,
 RA Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,
 RA Bell G.I.;
 RT "Genetic variation in the gene encoding calpain-10 is associated with
 RT type 2 diabetes mellitus.";
 RL Nat. Genet. 26:163-175(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -I- FUNCTION: Orphan receptor.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; AF200349; AAH18487.1; -; mRNA.
 DR EMBL; BC027429; AAH27429.1; -; mRNA.
 DR Ensembl; ENSMUSG00000026271; Mus musculus.
 DR MGI; MGI:1929509; Gpr35.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR InterPro; IPR002286; P2_puroceptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PRINTS; PR01157; P2YPUROCPTR.
 DR PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
 DR PROSITE; PS00262; G PROTEIN RECP F1_2; 1.

KW	G-protein coupled receptor; Glycoprotein; Receptor; Transducer; Transmembrane.	
KW	TOPO DOM	1
FT	Transmem	18
FT	Transmem	39
FT	TOPO DOM	53
FT	Transmem	54
FT	TOPO DOM	74
FT	Transmem	75
FT	TOPO DOM	88
FT	Transmem	89
FT	TOPO DOM	111
FT	Transmem	129
FT	TOPO DOM	130
FT	Transmem	150
FT	TOPO DOM	151
FT	Transmem	176
FT	TOPO DOM	177
FT	Transmem	197
FT	TOPO DOM	198
FT	Transmem	217
FT	TOPO DOM	238
FT	Transmem	218
FT	TOPO DOM	239
FT	Transmem	257
FT	TOPO DOM	258
FT	Transmem	278
FT	TOPO DOM	279
FT	CARBOHYD	2
FT	CARBOHYD	7
FT	DISULFID	87
SQ	SEQUENCE	307 AA; 34152 MW; OB3D02CECB16710D CRC64;
Query Match 69.6%; Score 1124; DB 1; Length 307;		
Best Local Similarity 71.9%; Pred. No. 3e-76;		
Matches 223; Conservative 30; Mismatches 51; Indels 6; Gaps 5;		
QY	1	MNGTYNTCGSSDLTPWPAIKLGFYALGVLLVGLLLNSLALWVFCRMOQWTEIRIYMT 60
DB	1	MNST--TCNST-LTPASVNNFFIYSALLLVGLLLNSLALWVFCYRHMOWTEIRIYMT 57
QY	61	NLAVALDCLLCTLPVFLHSR-DTSDTPLCQLSQGIYLTNRYSLSLTAIAVDRIYAVR 119
DB	58	NLAVALDCLLCSLPVFLYSKYSSTDPVCQLSQGIYLTNRYSLSLTAIAVDRIYAVR 117
QY	120	HPLRARGLRSPQAAAVCAVLWLVIGSLVARWLLGIQEGGCFPRS-TRHNFSMRFPIL 178
DB	118	HPLRARELRSPQAAAVCAVLWLVVTSLVVRWLGQMGQGGCFSSQTRNFSTTAFSL 177
QY	179	GYFLPLAVVFCSLKVTTALAQRPTDVQAEATKAAARMWVANLLVFCVCLPLHVLGT 238
DB	178	GYFLPLAIVFCSLQVTVLSRRPADVQAEATKATHMWANLAVFVICFLPLHVL 237
QY	239	VRLAVGNACALLETRIRALYITSLSDANCCLDACIYYMAKEFOEASALAVAPRAKAH 298
DB	238	VQVSLNLTCAARDTFSRALSITGKLSDTNCCLDACIYYMAKEFOEASALAVAPRAKAH 296
QY	299	KSQDSLCTVL 308
DB	297	KSQDSLCTVL 306
RESULT 8		
Q8CB97	MOUSE	PRELIMINARY; PRT; 307 AA.
ID	Q8CB97	MOUSE PRELIMINARY; PRT; 307 AA.
AC	Q8CB97	
DT	01-MAR-2003	(TrEMBLrel. 23, Created)
DT	01-MAR-2003	(TrEMBLrel. 23, Last sequence update)
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)
DE	Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830121M19 product:G protein-coupled receptor 35, full insert sequence.	
GN	Name=Gpr35;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;	
OC	Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=C57BL/6J; TISSUE=Bone;	
RX	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;	
RA	Carninci P., Hayashizaki Y.;	
RT	"High-efficiency full-length cDNA cloning.";	
RL	Meth. Enzymol. 303:19-44(1999).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=C57BL/6J; TISSUE=Bone;	
RX	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;	
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,	


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CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; CAAB01007335; CAF90112.1; -, Genomic_DNA.
DR InterPro; IPR002476; GPCR Rhodopsin.
DR DR InterPro; IPR002188; p2y5_purinoceptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOODPSN.
DR PRINTS; PRO1067; P2Y5ORPHANK.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 305 305
SQ SEQUENCE 305 AA; 34283 MW; E9F740AD3FF04F32 CRC64;

Query Match      25.9%; Score 417.5; DB 2; Length 305;
Best Local Similarity 34.6%; Pred. No. 2.4e-23;
Matches 106; Conservative 59; Mismatches 108; Indels 33; Gaps 10;

QY 6 NTCGSSDLTWPAPKLGIFYAYL-GVLLVLGLLLSLALWVFCCRQQQTETRIYNTNLAV 64
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 7 NETGMEDCGIDDSFKYNLYSVVVSYVFLGLITNCAALFVFCRKMENETTFMTNIAL 66
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 65 ADLCCLCTLPF-VLHSLRD--TSDDPLCQLSGIYLTVNRYSISLATVAIDRVYVVRHP 121
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 SDLVVFVFLPFVKFYTNVRHWHPFGGLCKVSGTAGTATITNYGSMLEFLTCISVDRLAIVYP 126
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 122 LRARGLRSPROAAACAVLWLVIIGLSVARMLLGTQEGGF-----CF-----RST 166
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 127 FRSRAIRTRRNAAVCYAAVWLTIWG-----GISVTFFSTINSTATTTCFEGSKST 179
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 167 RHNFNS---MRPLLGFYLPNAVVFCSLKVVTAQAQPDTVGQAETRKAAARMVWANL 223
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 180 WRTYLSKITITFIIEVGFLLPLIANVCSLSVLRTL-QRPVTVAHGCDSKRRVLRMLVHL 238
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 224 LVFVVVCFPLHVLGVTLVLAAGVNACAL--LETIREALY-ITSKLSDANCLDAICYYTMA 280
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QY 239 GIFLICFPYNSILEFLYALVRTQALSCGVERPARTPIITLCUATLNCLDPPVYYEFS 298
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 281 KEFQEA 286
Db   : : : :

QY 299 ESFQKS 304
Db   : : : :

RESULT 11
Q502U9 HUMAN
ID Q502U9 HUMAN PRELIMINARY; PRT; 370 AA.
AC Q502U9
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE G protein-coupled receptor 23.
GN Name=GPR23;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OX Homo.
OC NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=G-protein coupled receptors; DOI=10.1073/pnas.242603899;
RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA O'Dowd B.F., Nguyen T., Jung B.P., Marchese A., Cheng R., Heng H.H.Q.,
RA Kolakowski L.P. Jr., Lynch K.R., George S.R.;
RT "Cloning and chromosomal mapping of four putative novel human G-
RT protein-coupled receptor genes";
RL Gene 187:75-81(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Bohm S.K., Khitin L.M., Pavan D.P., Bunnett N.W.;
RL Submitted (JUL-1997) to the ENBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97366605; PubMed=9223435; DOI=10.1006/bbrc.1997.6895;
RA Janssens R., Boeynaems J.M., Godart M., Communi D.;
RT "Cloning of a human heptahelical receptor closely related to the P2Y5
RT receptor";
RL Biochem. Biophys. Res. Commun. 236:106-112(1997).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org)";
RL Submitted (MAY-2003) to the ENBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15772651; DOI=10.1038/nature03440;
RA Ross M.T., Grafham D.V., Coffey A.J., Scherer S., McKay K., Muzny D.,
RA Platzer M., Howell G.R., Burrows C., Bird C.P., Frankish A.,
RA Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R., Wen G.,
RA Jones M.C., Hultes M.E., Andrews T.D., Scott C.E., Searle S.,
RA Ramner J., Whitaker A., Deadman R., Carter N.P., Hunt S.E., Chen R.,
RA Cree A., Gunaratne P., Havlak P., Hodgson A., Metzker M.L.,
RA Richards S., Scott G., Steffen D., Sodergren E., Wheeler D.A.,
RA Worley K.C., Ainscough R., Ambrose K.D., Ansari-Lari M.A., Aradhy S.,
RA Ashwell R.I., Babbage A.K., Bagguley C.L., Ballabio A., Banerjee R.,
RA Barker G.E., Barlow K.F., Barrett I.P., Bates K.N., Beare D.M.,
RA Beasley H., Beasley O., Beck A., Bethel G., Blechschmidt K., Brady N.,
RA Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
RA Bruford E.A., Bunay C., Burch P., Burford D., Burgess J., Burrill W.,
RA Burton J., Bye J.M., Carder C., Carrel L., Chakro J., Chapman J.C.,
RA Chavez D., Chen G., Chen Y., Chen Z., Chinault C.,
RA Ciccodicola A., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
RA Clerc-Blankenburg K., Clifford K., Cobley V., Cole C.G., Conquer J.S.,
RA Corby N., Connor R.E., David R., Davies J., Davis C., Davis J.,
RA Delgado O., Deshazo D., Dhani P., Ding Y., Dinh H., Dodsworth S.,
RA Draper H., Dugan-Rocha S., Dunham A., Dunn M., Durbin K.J., Dutta I.,
RA Eades T., Ellwood M., Emery-Cohen A., Errington H., Evans K.L.,
RA Faulkner L., Francis F., Frankland J., Fraser A.E., Galgoczy P.,
RA Gilbert J., Gill R., Gloeckner G., Gregory S.G., Gribble S.,
RA Griffiths C., Grocock R., Gu Y., Gwilliam R., Hamilton C., Hart E.A.,
RA Hawes A., Heath P.D., Heitmann K., Hennig R., Hernandez J.,
RA Hinzmann B., Ho S., Hoffs M., Howden P.J., Huckle E.J., Hume J.,
RA Hunt P.J., Hunt A.R., Isherwood J., Jacob L., Johnson D., Jones S.,
RA de Jong P.J., Joseph S.S., Keenan S., Kelly S., Kershaw J.K., Khan Z.,
RA Kioschis P., Klages S., Knights A.J., Kosluka A., Kovar-Smith C.,
RA Laird G.K., Langford C., Lawlor S., Leversha M., Lewis L., Liu W.,
RA Lloyd C., Lloyd D.M., Louisedge H., Loveland J.E., Lovell J.D.,
RA Lozado R., Lu J., Lyne R., Ma J., Maheshwari M., Matthews L.H.,
RA McDowall J., McLaren S., McMurray A., Meidl P., Meitinger T.,
RA Milne S., Miner G., Mistry S.L., Morgan M., Morris S., Mueller I.,
RA Mullikin J.C., Nguyen N., Nordiek G., Nyakatura G., O'dell C.N.,
RA Okwuonu G., Palmer S., Pandian R., Parker D., Parrish J.,
RA Pasternak S., Patel D., Pearce A.V., Pearson D.M., Pelan S.E.,
RA Perez L., Porter K.M., Ramsey Y., Reichwald K., Rhodes S.,
RA Ridler K.A., Schllessinger D., Schueler M.G., Sehra H.K.,
RA Shaw-Smith C., Shen H., Sheridan E.M., Shownkeen R., Skuce C.D.,
RA Smith M.L., Sotheran E.C., Steingrubner H.E., Steward C.A., Storey R.,
RA Swann R.M., Swarbreck D., Tabor P.E., Taudien S., Taylor T.,
RA Teague B., Thomas K., Thorpe A., Timms K., Tracey A., Trevanion S.,
RA Tromans A.C., d'Urso M., Verduzco D., Villaseana D., Waldron L.,
RA Wall M., Wang Q., Warren J., Warry G.L., Wei X., West A.,
RA Whitehead S.L., Whitley M.N., Wilkinson J.E., Willey D.L.,
RA Williams G., Williams L., Williamson A., Williamson H., Wilming L.,
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RA Zorilla S., Buck D., Reinhardt R., Pouotka A., Rosenthal A.,
RA Lehrach R., Meindl A., Minx P.J., Hillier L.W., Willard H.F.,
RA Wilson R.K., Waterston R.H., Rice C.M., Vaudin M., Coulson A.,
RA Nelson D.L., Weinstock G., Sulston J.E., Durbin R., Hubbard T.,
RA Gibbs R.A., Beck S., Rogers J., Bentley D.R.;
RT "The DNA sequence of the human X chromosome";
RL Nature 434:325-337(2005).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Not detected in the brain regions thalamus,
CC putamen, caudate, frontal cortex, pons, hypothalamus and
CC hippocampus.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; U66578; AAC51301.1; -; Genomic DNA.
CC EMBL; U90323; AAB62087.1; -; Genomic DNA.
CC EMBL; U90322; AAB62088.1; -; mRNA.
CC EMBL; AF005419; AAB6322.1; -; Genomic DNA.
CC EMBL; AY301274; AAP58404.1; -; Genomic DNA.
CC EMBL; AL590083; CAD18851.1; -; Genomic DNA.
CC EMBL; BC074722; AAH74722.1; -; mRNA.
CC PIR; JC5549; JC5549.
CC HSPF; P34996; IDDD.
CC Ensembl; ENSG00000147145; Homo sapiens.
CC HGNC; HGNC:4478; GPR23.
CC MIM; 300086; -.
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0004930; P: G-protein coupled receptor activity; TAS.
CC GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; TAS.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC InterPro; IPR002188; P2Y5_purinocptor.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsn.
CC PRINTS; PR01067; P2Y5ORPHAN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
KW Transmembrane. 1 43 Extracellular (Potential).
FT TOPO_DOM 1 43
FT TRANSMEM 44 64 1 (Potential).
FT TOPO_DOM 65 73 Cytoplasmic (Potential).
FT TRANSMEM 74 94 2 (Potential).
FT TOPO_DOM 95 112 Extracellular (Potential).
FT TRANSMEM 113 133 3 (Potential).

GN Name=Gpr23;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakura I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
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RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Mazzarelli J., Mombaerts P.,
RA Lyons P., Marchionni L., Mashima J., Mazzaletti I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RN Genome Res. 10:1617-1630(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1757-1771(2000).
RN [6]

RA Hayaashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Kori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Oheato N., Okazaki Y.,
RA Saito R., Saiton H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL: AK051709; BAC34729.1; -, mRNA.
DR MGI: MGI:1925384; Gpr23.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0045028; F: purinergic nucleotide receptor activity; G- . .; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.
DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR GO: GO:0007165; P: signal transduction; IEA.
DR InterPro: IPR002188; GPCR_Rhodopsn.
DR InterPro: IPR002188; P2Y5_purinceptor.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PRINTS: PR01067; P2Y5ORPHAN.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; UNKNOWN_1.
DR PROSITE: PS00262; G-PROTEIN RECEPTOR FL2; 1.
DR PROSITE: PS00262; G-PROTEIN RECEPTOR; Transducer; Transmembrane.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 370 AA; 41956 MW; AB126842343AE6E1 CRC64;
Query Match 24.8%; Score 400; DB 2; Length 370;
Best Local Similarity 34.3%; Pred. No. 5.8e-22;
Matches 104; Conservative 59; Mismatches 112; Indels 28; Gaps 11;
Qy 4 TYNTGSSDLTPWPAIKLGFY-AVLGVLLVGLLNSLALWVFCRMOQWETRIYMTNL 62
Db 27 TNNTCI VDD-----SFTNNGAVSVVFLGLTNSASLFFCFMRKORSETAIFINL 81
Qy 63 AVADLCILCTLPF-VLHSLR---DTSPTPLCOLSQGIYLTNRYMSISLVTAIAVDYRVAV 118
Db 82 ALSDLLFVCTLPFKIFYNFNRHWPFGDT-LCKISCTAFLTNIYGSMLFLTCISVDRLAI 140
Qy 119 RHPRLARGLRSPROAAVCAVLVVLVIGSLVARWLLGQF-----GGCFSTRHN 169
Db 141 VYFPRSTRIRTRNSAIVCAGWILVNGGISLSTFTNNTNNATTTTCFGEFKRWKTY 200
Qy 170 FNSMR--PPLLGFLVPLAVVVCSSIKVVTALAQRPPTDVGQAEAT-RKAARVMANLVF 226
Db 201 LSKITIFIEVVGFIPLILNVSCSVLRTL--RKPATLSQIGTKKVKLVKMTYHMAVF 258
Qy 227 VVCFPLHVLGTLVRLAVGNAC--ALLETTIRRLY-ITSKLSDANCCLDAICYVMKEF 283
Db 259 VVCFVPYNSVLFYALVRSQAITNCLLRFKIMYPITCLATLNCCLDFPFYFTLESF 318
Qy 284 QEA 286
Db 319 QKS 321
RESULT 15
Q8BLG2 MOUSE
ID Q8BLG2 MOUSE PRELIMINARY; PRT; 370 AA.
AC Q8BLG2
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length
DE enriched library, clone:B130055L15 product:P2Y PURINOCEPTOR 9, full
DE insert sequence.
GN Name=Gpr23;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Maehima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohatsu S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX The PANTOM Consortium.
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-394-format
 sequencing pipeline with 384 multiplexed capillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akai S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL; AK045289; BAC32299.1; -, mRNA.
 DR Ensemble; ENSMUSG00000049929; Mus musculus.
 DR MGI; MGI:1925384; Gpr23.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0045028; P:purinergic nucleotide receptor activity; G-. . .; IEA.
 DR GO; GO:0004872; P:receptor activity; IEA.
 DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR002188; p2y5_purinoceptor.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PRINTS; PR01067; P2Y5ORPHAN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 370 AA; 41872 MW; 0E4C79FEDFD32050 CRC64;
 Query Match 24.3%; Score 392; DB 2; Length 370;
 Best Local Similarity 34.5%; Pred. No. 2.3e-21;
 Matches 97; Conservative 59; Mismatches 103; Indels 22; Gaps 9;
 QY 25 AVIGLVLLVGLLNSLALWVFCRQMQWTEIRYMTNLAVADCLLCITLPP-VLHSLR-- 81
 DB 44 AVISVFVILGLITSSASLFFVFCRMMKRSFAITNLALSLLPVCITLPPKIFNFRH 103
 QY 82 -DTSDTPLCQLSQGIYLTNRNYSISLVTAIAVDYVAVRHPRLRGLRSPRQAAAVCAVL 140
 DB 104 WFPQGT-LCKISGTAFNLNYGSMPLTICISVDREPLAIVYPPRSRTIRTRNSAIVCAGV 162
 QY 141 WVLVIGSLVARWLLGIQE-----GGPCFRSTRHNFNSMR--PPLIGFYPLAVVVF 189
 DB 163 WILVLSGGGISASLFPSTTVNNATTTFCFEGFSKRVKTYLSKITIFIEVVGFITLILNVS 222
 QY 190 CSLKVVTAALQRPPTDVQAEAT-RKAARMVWNLVVFVVCPLPLHVLGTVPLAVGMNAC 248
 DB 223 CSSVVLRTL--RKPATLSQIGTNKKKVLKMITVHMAVFCVCPVNSVLFLYLVRSQAI 280
 QY 249 --ALLETTIRRLY-ITSKLSDANCCCLDAICYMYMAKBFQEA 286
 DB 281 TWCLLERFAKIMYPITLCATLNCDFDPFIYFTLESFQKS 321
 Search completed: February 9, 2006, 01:00:17
 Job time : 168.5 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 00:47:19 ; Search time 214.5 Seconds
(without alignments)
632.951 Million cell updates/sec

Title: US-10-083-168-85

Perfect score: 1615

Sequence: 1 MNGTYTCGSSDLTWPPAIK.....AVAPRAKHKQSDSLCVTLA 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1615	100.0	309	5	ABG95172 Human GPC
2	1609	99.6	309	3	AAY79576 Human G p
3	1609	99.6	309	5	ABG95159 Human GPC
4	1609	99.6	309	6	ABP82002 Human G p
5	1609	99.6	309	7	ADB67656 Human G p
6	1609	99.6	309	8	ADO29394 Human GPC
7	1609	99.6	309	8	ADO78094 Human GPR
8	1609	99.6	309	9	ADV73203 Human col
9	1609	99.6	309	9	ABE15039 Human GPR
10	1603	99.3	309	3	AAY69989 Human rec
11	1603	99.3	309	7	ADP70461 Orphan re
12	1601	99.1	309	7	ADP50511 Human GPC
13	1597	98.9	309	3	AAY58645 Human G-p
14	1597	98.9	309	6	ADA84069 Human GPR
15	1597	98.9	394	8	ADO78095 Human GPR
16	1597	98.9	394	8	ADR10454 Human pro
17	1377	85.3	286	8	ADP29765 Human sec
18	1123	63.5	307	8	ADO29395 Mouse GPC
19	401	24.8	370	2	AAW62597 Human 7-t
20	401	24.8	370	5	ABP61511 Human NF-
21	401	24.8	370	6	ABG73513 Human p2y
22	401	24.8	370	6	ABP81870 Human G p
23	401	24.8	370	7	ADH69286 Human pur
24	401	24.8	370	8	ADF91778 Human p2y

25	401	24.8	370	8	ADO29049	Ado29049 Human nov
26	401	24.8	370	8	ADQ88244	Adq88244 Human 241
27	401	24.8	370	8	ADQ81575	Adq81575 Human iye
28	401	24.8	370	8	ADs84260	Ads84260 Human G p
29	401	24.8	370	9	ADV35123	Adv35123 Human tra
30	401	24.8	608	7	ADF70491	Adf70491 Orphan re
31	400	24.8	370	7	ADH69285	Adh69285 Human pur
32	400	24.8	370	8	ADF91777	Adf91777 Human p2y
33	396	24.5	370	5	ADO29050	Ado29050 Mouse nov
34	391	24.2	370	5	ABP61510	Abp61510 Human NF-
35	389	24.1	368	8	ADs84259	Ads84259 Human G p
36	388	24.0	327	8	ADO29415	Ado29415 Mouse GPC
37	382.5	23.7	363	9	ADM44804	Adm44804 Human RUP
38	382.5	23.7	363	9	ADM44778	Adm44778 Human EPA
39	382.5	23.7	363	9	ABE20962	Aeb20962 Human RUP
40	381.5	23.6	363	9	ADM44818	Adm44818 Human RUP
41	381.5	23.6	363	9	ADM44796	Adm44796 Human RUP
42	380.5	23.6	363	9	ADM44807	Adm44807 Human RUP
43	379.5	23.5	363	9	ADM44802	Adm44802 Human RUP
44	378.5	23.4	363	9	ADM44810	Adm44810 Human RUP
45	378.5	23.4	363	9	ADM44805	Adm44805 Human RUP

ALIGNMENTS

RESULT 1

ABG95172

ID ABG95172 standard; protein; 309 AA.

XX AC ABG95172;

XX AC

DT 04-DEC-2002 (first entry)

XX Human GPCR GPR35 mutant A216K.

DE Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;

XX Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;

XX Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;

KW hypertensive; reflux disease; depression; migraine; schizophrenia; ulcer;

KW psychotonic disorder; asthma; bronchospasm; anaesthesia;

KW myocardial infarction; MI; stroke; glaucoma; anxiety;

KW prostatic hypertrophy; epilepsy; prostate cancer; rhinitis; angina;

KW prostatic hypertrophy; receptor; mutant; mutin.

XX Homo sapiens.

OS Synthetic.

XX WO200268600-A2.

XX WO200268600-A2.

XX 06-SEP-2002.

PD 06-SEP-2002.

XX 26-FEB-2002; 2002WO-US005625.

XX 26-FEB-2001; 2001US-0271913P.

XX (AREN-) ARENA PHARM INC.

PA Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;

XX Lin I, Ortuno D;

XX WPI; 2002-706980/76.

DR N-PSDB; ABS73401.

XX New human G-protein coupled receptor (GPCR), useful for screening agonist

XX or inverse agonist compounds for treating diseases associated with GPCR.

PS Example 2; Page 189-190; 201pp; English.

XX The present invention relates to transmembrane receptors, particularly

CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-

CC endogenous) versions of the GPCRs, and the polynucleotide sequences

CC encoding them. The GPCRs are useful for screening agonist or inverse

CC agonist compounds for treating diseases associated with GPCR. Diseases

CC that can be treated with such compounds include allergies, hypertension,

CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic
CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),
CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,
CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present
XX sequence represents a mutant human GPCR
SQ Sequence 309 AA;

Query Match 100.0%; Score 1615; DB 5; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.6e-168;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFAVYLVGLVLLGILLNSLALWVFCRMOQWTTETRIYMT 60
DB 1 MNGTYNTCGSSDLTWPPAIKLGFAVYLVGLVLLGILLNSLALWVFCRMOQWTTETRIYMT 60

QY 61 NLAVADLCCLCTLPFVHLHSRLDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDVYVAVRH 120
DB 61 NLAVADLCCLCTLPFVHLHSRLDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDVYVAVRH 120

QY 121 PLRARGLSRPROAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRHNFNSMRPPLG 180
DB 121 PLRARGLSRPROAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRHNFNSMRPPLG 180

QY 181 YLPLAVVVFCSLKVVTALAQRPTDVGOAEATRKAKRWANLLVFPVCFPLPHVGLTVR 240
DB 181 YLPLAVVVFCSLKVVTALAQRPTDVGOAEATRKAKRWANLLVFPVCFPLPHVGLTVR 240

QY 241 LAVGNACALLETIRRALYITTSKLSANCCCLDAICYYNMAKEFQASALAVAPRAKAHKS 300
DB 241 LAVGNACALLETIRRALYITTSKLSANCCCLDAICYYNMAKEFQASALAVAPRAKAHKS 300

QY 301 QDSLVCVTLA 309
DB 301 QDSLVCVTLA 309

RESULT 2
ID AAY79576 standard; protein; 309 AA.
XX
AC AAY79576;
XX
DT 15-AUG-2000 (first entry)
DE Human G protein coupled receptor GPR35.
XX
KW GPR35; G protein coupled receptor; human; NIDDM1;
KW non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10;
KW diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 174 /note= "encoded by GCG"
FT Misc-difference 294 /note= "encoded by AGT"
XX
PN WO200023603-A2.
XX
PD 27-APR-2000.
XX
PF 21-OCT-1999; 99WO-US024890.
XX
PR 21-OCT-1998; 98US-0105052P.
PR 13-MAY-1999; 99US-0134175P.
XX
XX (ARCH-) ARCH DEV CORP.
XX (TEXA) UNIV OF TEXAS SYSTEM.
XX Polonsky KS, Horikawa Y, Oda N, Sreenan S, Zhou Y, Otani K;
PI Hanis CL, Bell GI, Cox NJ;

XX
DR WPI; 2000-339702/29.
DR N-PSDB; AAA27485, AAY79574, AAY79576.
XX
PT Method for screening for type 2 diabetes mellitus comprises detecting a
PT polymorphism in a calpain encoding nucleic acid segment or a protease-
PT encoding nucleic acid segment.
XX
PS Claim 75; Page 237-238; 257pp; English.
XX
CC The present sequence is that of the human gene encoding G protein coupled
CC receptor, GPR35 as deduced from a composite cDNA (see AAA27485). The
CC sequence of GPR35 is similar to that of a putative purinoceptor P2Y9
CC (34.1% identity) suggesting that ATP or other nucleotide is its ligand.
CC GPR35 mRNA was detected in all adult and foetal tissues examined with
CC relatively higher levels in adult lung, small intestine, colon and
CC stomach. In these tissues, there are 2 major transcripts of 2.4 and 4.4
CC kb, whereas in skeletal muscle there is a single transcript of 9.4 kb.
CC The GPR35 gene is located in a 49,136 bp region (see AAA27475) within the
CC NIDDM1 region of human chromosome 2. This region also includes the CAPN10
CC gene, which encodes a novel calpain-like cysteine protease, designated
CC calpain 10. Mutations in the CAPN10 gene are responsible for a
CC susceptibility to type 2 diabetes. Claimed methods for screening for a
CC propensity for type 2 diabetes mellitus are based on detection of a
CC polymorphism in a calpain encoding nucleic acid. Methods are also claimed
CC for identifying modulators of calpain activity, and using these
CC modulators to treat diabetes, in particular through the regulation of an
CC insulin secretory response or insulin mediated glucose transport
XX
SQ Sequence 309 AA;

Query Match 99.6%; Score 1609; DB 3; Length 309;
Best Local Similarity 99.7%; Pred. No. 1.2e-167;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFAVYLVGLVLLGILLNSLALWVFCRMOQWTTETRIYMT 60
DB 1 MNGTYNTCGSSDLTWPPAIKLGFAVYLVGLVLLGILLNSLALWVFCRMOQWTTETRIYMT 60

QY 61 NLAVADLCCLCTLPFVHLHSRLDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDVYVAVRH 120
DB 61 NLAVADLCCLCTLPFVHLHSRLDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDVYVAVRH 120

QY 121 PLRARGLSRPROAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRHNFNSMRPPLG 180
DB 121 PLRARGLSRPROAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRHNFNSMRPPLG 180

QY 181 YLPLAVVVFCSLKVVTALAQRPTDVGOAEATRKAKRWANLLVFPVCFPLPHVGLTVR 240
DB 181 YLPLAVVVFCSLKVVTALAQRPTDVGOAEATRKAKRWANLLVFPVCFPLPHVGLTVR 240

QY 241 LAVGNACALLETIRRALYITTSKLSANCCCLDAICYYNMAKEFQASALAVAPRAKAHKS 300
DB 241 LAVGNACALLETIRRALYITTSKLSANCCCLDAICYYNMAKEFQASALAVAPRAKAHKS 300

QY 301 QDSLVCVTLA 309
DB 301 QDSLVCVTLA 309

RESULT 3
ABG95159
ID ABG95159 standard; protein; 309 AA.
XX
AC ABG95159;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human GPCR GPR35.
XX
KW Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;
KW hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;
KW psychotic disorder; asthma; bronchospasm; anaesthesia;

KW myocardial infarction; MI; stroke; glaucoma; anxiety;
KW prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;
KW prostatic hypertrophy; receptor.
XX
OS Homo sapiens.
XX
XX WO200268600-A2.
XX
XX 06-SEP-2002.
XX
XX 26-FEB-2002; 2002WO-US005625.
XX
XX 26-FEB-2001; 2001US-0271913P.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;
XX Lin I, Ortuno D;
XX
XX WPI; 2002-706980/76.
XX N-PSDB; ABS73345.
XX
XX New human G-protein coupled receptor (GPCR), useful for screening agonist
XX or inverse agonist compounds for treating diseases associated with GPCR.
XX
XX Claim 29; Page 128-130; 201pp; English.
XX
XX The present invention relates to transmembrane receptors, particularly
XX endogenous human G-protein coupled receptors (GPCRs), mutant (non-
XX endogenous) versions of the GPCRs, and the polynucleotide sequences
XX encoding them. The GPCRs are useful for screening agonist or inverse
XX agonist compounds for treating diseases associated with GPCR. Diseases
XX that can be treated with such compounds include allergies, hypertension,
XX reflux disease, depression, migraine, schizophrenia, ulcers, psychotic
XX disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),
XX stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,
XX anxiety, prostatic hypertrophy, rhinitis, and angina. The present
XX sequence represents an endogenous human GPCR
XX
SQ Sequence 309 AA;

Query Match 99.6%; Score 1609; DB 5; Length 309;
Best Local Similarity 99.7%; Pred. No. 1.2e-167;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNGTYNTCGSSDLTPPPAIIKLGFYAYLGVLLVGLLNSLALWVCCRMQQTETRIYMT 60
DB 1 MNGTYNTCGSSDLTPPPAIIKLGFYAYLGVLLVGLLNSLALWVCCRMQQTETRIYMT 60
QY 61 NLAVALDCLLCTLPFLVLSLRTSDTPIQLSQGIYLTNRYSISLVTAIAVDVAVVRH 120
DB 61 NLAVALDCLLCTLPFLVLSLRTSDTPIQLSQGIYLTNRYSISLVTAIAVDVAVVRH 120
QY 121 PLRAGRLSPROAAVCAVLVVLVIGSLVARMLLGIQGGFCFRTRNFNSMRPPLLGF 180
DB 121 PLRAGRLSPROAAVCAVLVVLVIGSLVARMLLGIQGGFCFRTRNFNSMRPPLLGF 180
QY 181 YLPLAVVFCSLKVTALAQRPPTDVGQAEATRKARVMWVNLVYVVCFFIPAHVGLTVR 240
DB 181 YLPLAVVFCSLKVTALAQRPPTDVGQAEATRKARVMWVNLVYVVCFFIPAHVGLTVR 240
QY 241 LAVGNACALLTIRRALYITSKLSDANCCDAICYTMAKEFQESALAVAPRAKAHS 300
DB 241 LAVGNACALLTIRRALYITSKLSDANCCDAICYTMAKEFQESALAVAPRAKAHS 300
QY 301 QDSLCVTLA 309
DB 301 QDSLCVTLA 309

RESULT 4
ABP82002
ID ABP82002 standard; protein; 309 AA.

XX
AC ABP82002;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human G protein-coupled receptor GPR35 protein SEQ ID NO:492.
XX
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW psoriasis; anxiety; depression; Parkinson's disease; multiple sclerosis; pain;
KW graft versus host disease; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
XX Homo sapiens.
XX OS
XX WO200261087-A2.
XX PN
XX 08-AUG-2002.
XX PD
XX 19-DEC-2001; 2001WO-US050107.
XX PF
XX 19-DEC-2000; 2000US-0257144P.
XX PR
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX PA
XX Burmer GC, Roush CL, Brown JP;
XX WPI; 2003-046718/04.
XX DR N-PSDB; ABZ42852.
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.
XX
XX Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (I) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (I) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related diseases, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the
XX exemplification of the present invention
XX
SQ Sequence 309 AA;

Query Match 99.6%; Score 1609; DB 6; Length 309;
Best Local Similarity 99.7%; Pred. No. 1.2e-167;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTTETRIYMT 60
DB 1 MNGTYNTCGSSDLTPWPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTTETRIYMT 60
QY 61 NLAVADLCCLLCTLPFVLSLRDTSPTPLCQLSGIYLTNRYSISLVTAIAVDVRYAVRH 120
DB 61 NLAVADLCCLLCTLPFVLSLRDTSPTPLCQLSGIYLTNRYSISLVTAIAVDVRYAVRH 120
QY 121 PLRARGLSRPRQAAACAVLWLVIGSLVARMLLGIQEGGFCFRSTRHNFNSRFPPLG 180
DB 121 PLRARGLSRPRQAAACAVLWLVIGSLVARMLLGIQEGGFCFRSTRHNFNSRFPPLG 180
QY 181 YLPLAVVFCSLKVVTALAQRPTDVQAEATRKAKRMVWVANLLVFWVCFPLHVGLTVR 240
DB 181 YLPLAVVFCSLKVVTALAQRPTDVQAEATRKAKRMVWVANLLVFWVCFPLHVGLTVR 240
QY 241 LAVGNACALLETTIRRALYITSKLSDANCLDAICYNNMAKFOEASALAVAPRAKAHKS 300
DB 241 LAVGNACALLETTIRRALYITSKLSDANCLDAICYNNMAKFOEASALAVAPRAKAHKS 300
QY 301 QDSLVCVTLA 309
DB 301 QDSLVCVTLA 309

RESULT 5

ADB67656
ID ADB67656 standard; protein; 309 AA.
XX ADB67656;
AC ADB67656;
DT 04-DEC-2003 (first entry)
DE Human G protein-coupled receptor 35, SEQ ID 25.
XX Cardiant; Gene therapy; heart failure; human;
KW G protein-coupled receptor 35; receptor.
XX Homo sapiens.
OS WO2003072824-A1.
PN 04-SEP-2003.
PD 27-FEB-2003; 2003WO-JP002228.
PF 28-FEB-2002; 2002JP-00054388.
PR 15-APR-2002; 2002JP-00112228.
XX (SANY) SANKYO CO LTD.
XX Kitakaze M, Takashima S, Asakura M, Isomura T, Furukawa H;
PI Koishi R, Nakamaru K;
XX WPI; 2003-679959/64.
DR N-PSDB; ADB67672.
XX Predicting pathological conditions in heart failure using marker genes
and proteins.
XX Claim 1; Page 111-113; 137pp; Japanese.
XX The present invention relates to a method for predicting pathological
conditions in heart failure using expression of one of 17 gene sequences
(ADB67663-ADB67678); or protein sequences encoded by the genes (ADB67648-
ADB67662). The proteins and genes are useful for diagnosis, treatment and
prevention of heart failure.
XX Sequence 309 AA;
SQ Query Match 99.6%; Score 1609; DB 7; Length 309;

Best Local Similarity 99.7%; Pred. No. 1.2e-167;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTTETRIYMT 60
DB 1 MNGTYNTCGSSDLTPWPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTTETRIYMT 60
QY 61 NLAVADLCCLLCTLPFVLSLRDTSPTPLCQLSGIYLTNRYSISLVTAIAVDVRYAVRH 120
DB 61 NLAVADLCCLLCTLPFVLSLRDTSPTPLCQLSGIYLTNRYSISLVTAIAVDVRYAVRH 120
QY 121 PLRARGLSRPRQAAACAVLWLVIGSLVARMLLGIQEGGFCFRSTRHNFNSRFPPLG 180
DB 121 PLRARGLSRPRQAAACAVLWLVIGSLVARMLLGIQEGGFCFRSTRHNFNSRFPPLG 180
QY 181 YLPLAVVFCSLKVVTALAQRPTDVQAEATRKAKRMVWVANLLVFWVCFPLHVGLTVR 240
DB 181 YLPLAVVFCSLKVVTALAQRPTDVQAEATRKAKRMVWVANLLVFWVCFPLHVGLTVR 240
QY 241 LAVGNACALLETTIRRALYITSKLSDANCLDAICYNNMAKFOEASALAVAPRAKAHKS 300
DB 241 LAVGNACALLETTIRRALYITSKLSDANCLDAICYNNMAKFOEASALAVAPRAKAHKS 300
QY 301 QDSLVCVTLA 309
DB 301 QDSLVCVTLA 309

RESULT 6
ADO29394
ID ADO29394 standard; protein; 309 AA.
XX ADO29394;
AC ADO29394;
DT 29-JUL-2004 (first entry)
DE Human GPCR GPR35, SEQ ID NO:496.
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytostatic; antiinflammatory; vasotropic; antidiabetic; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW receptor.
XX Homo sapiens.
OS WO2004040000-A2.
XX 13-MAY-2004.
XX 09-SEP-2003; 2003WO-US028226.
XX 09-SEP-2002; 2002US-0409303P.
PR 09-APR-2003; 2003US-0461329P.
XX (PRIM-) PRIMAL INC.
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX WPI; 2004-390329/36.
DR N-PSDB; ADO29916.


```
Db          301 QDSLCVTLA 309
|||||
RESULT 8
ADV73203
ID ADV73203 standard; protein; 309 AA.
XX
AC ADV73203;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human colon tumor cell upregulated protein SEQ ID NO 44.
XX
KW cancer; neoplasm; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004110345-A2.
XX
PD 23-DEC-2004.
XX
PF 28-OCT-2003; 2003WO-US034019.
XX
PR 29-OCT-2002; 2002US-0422176P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Bourner MJ, Bu JJ, Head RD, Hippenmeyer PJ, Klein BK;
P1 Mazzarella RA, Staten NR;
XX
XX WPI; 2005-039958/04.
DR N-PSDB; ADV73165.
XX
XX New antibody that immunospecifically binds to p-cadherin, useful in
PT preparing a composition for treating or preventing a cancer-associated
PT disorder.
XX
PS Disclosure; SEQ ID NO 44; 257pp; English.
XX
XX The invention relates to an antibody immunospecifically binds to p-
CC cadherin or its fragment. The antibody is useful in preparing a
CC composition for treating or preventing a cancer-associated disorder. The
CC present sequence represents the amino acid sequence of a protein
CC upregulated in human colon cancer cells.
XX
SQ Sequence 309 AA;
Query Match          99.6%; Score 1609; DB 9; Length 309;
Best Local Similarity 99.7%; Pred. No. 1.2e-167;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNGTYNTCGSSDLTWPPAIIKGFYAVILGVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
Db 1 MNGTYNTCGSSDLTWPPAIIKGFYAVILGVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
QY 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCQLSGGIYLTNRYSISLVTAIAVDYVAVRH 120
Db 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCQLSGGIYLTNRYSISLVTAIAVDYVAVRH 120
QY 121 PLRARGLRSPQAAACAVLWLVIGSLVARWLLGTOEGGFCFRSTRHFNFSMRFPILGF 180
Db 121 PLRARGLRSPQAAACAVLWLVIGSLVARWLLGTOEGGFCFRSTRHFNFSMRFPILGF 180
QY 181 YLPLAVVVFCSLKVVTALAQRPDVGQAEATKAKRWYMANLLVPVVCFLPLHVLGLTVR 240
Db 181 YLPLAVVVFCSLKVVTALAQRPDVGQAEATKAKRWYMANLLVPVVCFLPLHVLGLTVR 240
QY 241 LAVGNACALLETIRRALYITSKLSDANCLDAICYNNYMAKFEQASALAVAPRAKAHKS 300
Db 241 LAVGNACALLETIRRALYITSKLSDANCLDAICYNNYMAKFEQASALAVAPRAKAHKS 300
QY 301 QDSLCVTLA 309
|||||
Db          301 QDSLCVTLA 309
|||||
RESULT 9
AEB15039
ID AEB15039 standard; protein; 309 AA.
XX
AC AEB15039;
XX
DT 08-SEP-2005 (first entry)
XX
DE Human GPR35 polypeptide.
XX
KW G-protein coupled receptor 35; GPR35; G-protein coupled receptor; GPCR;
KW screening; cardiovascular disease; gastrointestinal disease;
KW liver disease; cancer; neoplasm; metabolic disorder;
KW hematological disease; respiratory disease; inflammation;
KW neurological disease; urological disorder; cardiovascular-gen.;
KW gastrointestinal-gen.; hepatotropic; cytostatic; metabolic; antianemic;
KW respiratory-gen.; antiinflammatory; neuroprotective; uropathic; receptor.
XX
OS Homo sapiens.
XX
PN WO2005059546-A2.
XX
PD 30-JUN-2005.
XX
PF 02-DEC-2004; 2004WO-EP013679.
XX
PR 12-DEC-2003; 2003EP-00028614.
XX
PA (FARB ) BAYER HEALTHCARE AG.
XX
PI Golz S, Brueggemeier U, Geerts A, Summer H;
XX
XX WPI; 2005-506223/51.
DR N-PSDB; AEB15038.
XX
XX Screening of therapeutic agents useful in treating specified diseases
PT involves contacting test compound with G-protein coupled receptor GPR35,
PT and detect binding of test compound to polypeptide.
XX
PS Disclosure; SEQ ID NO 2; 96pp; English.
XX
XX The invention relates to the use of human G-protein coupled receptor 35
CC (GPR35) for screening therapeutic agents useful in the treatment of
CC cardiovascular disorders, liver and gastrointestinal diseases, cancer
CC disorders, inflammatory diseases, metabolic diseases, hematological
CC disorders, respiratory diseases, neurological disorders and urological
CC disorders, in a mammal. GPR35 is a G-protein coupled receptor (GPCR). The
CC therapeutic agents are screened by contacting a test compound with GPR35
CC polypeptide, and detecting the binding of the test compound to the
CC polypeptide. Also described are: (1) a method of diagnosing the above
CC specified diseases in a mammal, comprising determining the amount of a
CC GPR35 polynucleotide in a sample taken from the mammal, and determining
CC the amount of the GPR35 polynucleotide in healthy and/or diseased mammals
CC; (2) a pharmaceutical composition for treating the above specified
CC diseases in the mammal, comprising a therapeutic agent that binds to the
CC GPR35 polypeptide; (3) use of regulators of a GPR35 for the preparation
CC of the pharmaceutical composition or for the regulation of GPR35 activity
CC in a mammal having the above specified diseases; and (4) a method for the
CC preparation of the pharmaceutical composition, comprising identifying the
CC GPR35 regulator, determining whether the regulator ameliorates the
CC symptoms of the above specified diseases in a mammal, and combining the
CC regulator with an acceptable pharmaceutical carrier. GPR35 is useful for
CC screening therapeutic agents for treating cardiovascular disorders, liver
CC and gastrointestinal diseases, cancer disorders, inflammatory diseases,
CC metabolic diseases, hematological disorders, respiratory diseases,
CC neurological disorders and urological disorders in a mammal, e.g. humans
CC (preferably), dogs, cats, cows, horses, rabbits, and monkeys. This
CC sequence represents human GPR35.
```

[illegible]

```
RESULT 11
ADF70461
ID ADF70461 standard; protein; 547 AA.
XX
AC ADF70461;
XX
DT 12-FEB-2004 (first entry)
XX
DE Orphan receptor ligand-related human protein SeqID84.
XX
KW ligand; orphan receptor protein; fusion protein; fluorescent protein;
KW cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
KW GFPuv; Enhanced GFP; EGFP; human.
XX
OS Homo sapiens.
XX
PN WO2003071272-A1.
XX
PD 28-AUG-2003.
XX
PF 21-FEB-2003; 2003WO-JP001901.
XX
PR 22-FEB-2002; 2002JP-00045728.
XX
PR 23-JUL-2002; 2002JP-00213949.
XX
PR 11-OCT-2002; 2002JP-00298237.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;
PI WPI; 2003-697654/66.
DR N-PSDB; ADF70563.
XX
PT Transformation of cells with a fusion protein of an orphan receptor
PT protein with a fluorescent protein useful for identification of ligands
PT to the orphan receptor.
XX
PS Disclosure; SEQ ID NO 84; 594pp; Japanese.
XX
CC This invention relates to a novel method of identifying ligands to an
CC orphan receptor protein which comprises transforming cells with DNA
CC encoding a fusion protein of the orphan receptor with a fluorescent
CC protein, so that the fusion protein is expressed in the cells (or cell
CC membranes isolated from them) and contacting the cells with the potential
CC ligand to be tested. A suitable fluorescent protein for incorporation in
CC the fusion protein is green fluorescent protein (GFP), for example GFP-1,
CC wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the
CC identification of ligands binding to an orphan receptor protein.
XX
SQ Sequence 547 AA;
Query Match 99.3%; Score 1603; DB 7; Length 547;
Best Local Similarity 99.4%; Pred. No. 1.1e-166;
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MNGTYNTCGSSDLTWPAPKLGFPAYLVGLVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
DB 1 MNGTYNTCGSSDLTWPAPKLGFPAYLVGLVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
QY 61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTAIADRVYAVRH 120
DB 61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYSISLVTAIADRVYAVRH 120
QY 121 PLRARGLSRQAAACAVLWLVLSVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF 180
DB 121 PLRARGLSRQAAACAVLWLVLSVARWLLGIQEGGFCFRSTRHNFNSMRFPLLGF 180
QY 181 YLPVAVVFCSLKVVTALLQRPPTDVGQAEATKAKRMVWVANLLVFWVCFPLHVLGTVR 240
DB 181 YLPVAVVFCSLKVVTALLQRPPTDVGQAEATKAKRMVWVANLLVFWVCFPLHVLGTVR 240
QY 241 LAVGNACALLETTIRREALYITSKLSDANCCCLDAICYYVNAKEFQEQASALAVAPRAKAHKS 300
DB 241 LAVGNACALLETTIRREALYITSKLSDANCCCLDAICYYVNAKEFQEQASALAVAPRAKAHKS 300
QY 301 QBSLCVTLA 309
DB 301 QBSLCVTLA 309
RESULT 12
ADF50511
ID ADF50511 standard; protein; 309 AA.
XX
AC ADF50511;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human GPCR GPR35 D113A mutein (SeqID 191).
XX
KW mutant; mutein; transformation; endocrine cell line;
KW expression cloning system; bioactive peptide; GPCR ligand; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 113 /note= "Wild type Asp substituted by Ala"
XX
PN WO2003087366-A1.
XX
PD 23-OCT-2003.
XX
PF 16-APR-2003; 2003WO-JP004840.
XX
PR 16-APR-2002; 2002JP-00113030.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Sasaki K, Miura K, Saeki S, Yoshizawa M, Kishimoto K, Kunitomo H;
PI Nishi T, Obinata M;
XX
WPI; 2003-833737/77.
XX
DE Endocrine cell lines originated from mammalian hypothalamus and
PT pancreatic islet, applicable in expression cloning systems of bioactive
PT peptide precursor genes, and in screening G protein-coupled receptor
PT ligands.
XX
PS Example 24; SEQ ID NO 191; 316pp; Japanese.
XX
CC This invention relates to a novel method for obtaining a DNA that encodes
CC a peptide acting as agonist, antagonist or inverse agonist on a target
CC receptor. Specifically, it comprises transformation of endocrine cell
CC lines originating from mammalian hypothalamus and pancreatic islets,
CC culturing the transformants and contacting with cells expressing the
CC target receptor. The identification of those cells with a response
CC reaction can be used for selecting a transformant cell line with the
CC appropriate target activity that is expressing the novel transformed DNA.
CC Accordingly, the present invention describes novel cell lines that are
CC applicable in expression cloning systems of bioactive peptide precursor
CC genes, and in screening GPCR ligands for use as drugs including agonists,
CC antagonists and inverse agonists i.e. activators and inhibitors. Such
CC cell lines can provide a highly sensitive and convenient GPCR ligand
CC assay system. This polypeptide sequence is the human GPCR GPR35 D113A
XX
SQ Sequence 309 AA;
Query Match 99.1%; Score 1601; DB 7; Length 309;
Best Local Similarity 99.4%; Pred. No. 8.9e-167;
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MNGTYNTCGSSDLTWPAPKLGFPAYLVGLVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
DB 1 MNGTYNTCGSSDLTWPAPKLGFPAYLVGLVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
```

Db 1 MNGTYNTGSSDITWPPAIGFYAVLGVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
 QY 61 NLAVADICLLCTLPFVLSLRDSDTLPCLQSOGIYLTNRYMSISLVTAADRYAVRH 120
 Db 61 NLAVADICLLCTLPFVLSLRDSDTLPCLQSOGIYLTNRYMSISLVTAADRYAVRH 120
 QY 121 PLRARGLSRQAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRHNFNSMRFPPLGF 180
 Db 121 PLRARGLSRQAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRHNFNSMRFPPLGF 180
 QY 181 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRAKRWANLIVFVVCFLPLHVLTVR 240
 Db 181 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRAKRWANLIVFVVCFLPLHVLTVR 240
 QY 241 LAVGWNA CALLETIRRALYITSKLSANDCCCLDAICYYYMAKEFOEASALAVAPRAKAHS 300
 Db 241 LAVGWNA CALLETIRRALYITSKLSANDCCCLDAICYYYMAKEFOEASALAVAPRAKAHS 300
 QY 301 QDSLVCVTLA 309
 Db 301 QDSLVCVTLA 309

RESULT 13
 AAY58645
 ID AAY58645 standard; protein; 309 AA.
 AC AAY58645;
 XX
 DT 11-APR-2000 (first entry)
 XX
 DE Human G-protein coupled receptor GPR35A.
 XX
 KW GPR35A; human; G-protein coupled receptor; purinergic;
 KW 7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic;
 KW cytosolic; antidiabetic; anorectic; antiasthmatic; antiparkinsonian;
 KW hypotensive; hypertensive; osteopathic; antiangiinal; cardiant;
 KW cerebroprotective; antitumor; aniallergic; antimigraine; antiemetic;
 KW tranquilizer; antidepressant; neuroleptic; nootropic; anticonvulsant;
 KW therapy; diagnosis; vaccine.
 XX
 OS Homo sapiens.
 XX
 XX WO9964452-A1.
 XX
 XX 16-DEC-1999.
 XX
 XX 01-JUN-1999; 95WO-US012123.
 XX
 XX 11-JUN-1998; 98US-00096031.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 XX Elshourbagy NA;
 XX
 XX WPI; 2000-116525/10.
 XX
 XX N-PSDB; AAZ35390.
 XX
 XX New human GPR35A polypeptides and polynucleotides used to identify
 XX agonists, antagonists and inhibitors for use in therapy.
 XX
 XX Claim 1; Page 32-33; 38pp; English.
 XX
 XX The present sequence represents human GPR35A, a novel member of the
 XX purinergic family of polypeptides and a G-protein coupled receptor. The
 XX invention provides GPR35A polypeptides having at least 70% identity with
 XX the present sequence, GPR35A polynucleotides, recombinant materials, and
 XX methods for their production. GPR35A polypeptides can be used for
 XX identifying agonists and antagonists/inhibitors, and for detecting
 XX diseases associated with inappropriate GPR35A activity or levels. GPR35A
 XX polypeptides and polynucleotides, agonists, antagonists and antibodies
 XX are used to treat infections such as bacterial, fungal, protozoan and
 XX viral infections, particularly HIV-1 and HIV-2; pain; cancer; diabetes;

CC obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart
 CC failure; hypotension; hypertension; urinary retention; osteoporosis;
 CC angina pectoris; myocardial infarction; stroke; ulcers; allergy; benign
 CC prostatic hypertrophy; migraine; vomiting; psychotic and neurological
 CC disorders including anxiety, schizophrenia, manic depression, depression,
 CC delirium, dementia and severe mental retardation; and dyskinesias such as
 CC Huntington's or Gilles de la Tourette's syndrome. The polypeptide is also
 CC useful for production of vaccines
 XX
 SQ Sequence 309 AA;
 Query Match 98.9%; Score 1597; DB 3; Length 309;
 Best Local Similarity 99.0%; Pred. No. 2.5e-166;
 Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MNGTYNTGSSDITWPPAIGFYAVLGVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
 Db 1 MNGTYNTGSSDITWPPAIGFYAVLGVLLVGLLNSLALWVFCRMOQWTETRIYMT 60
 QY 61 NLAVADICLLCTLPFVLSLRDSDTLPCLQSOGIYLTNRYMSISLVTAADRYAVRH 120
 Db 61 NLAVADICLLCTLPFVLSLRDSDTLPCLQSOGIYLTNRYMSISLVTAADRYAVRH 120
 QY 121 PLRARGLSRQAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRHNFNSMRFPPLGF 180
 Db 121 PLRARGLSRQAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRHNFNSMRFPPLGF 180
 QY 181 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRAKRWANLIVFVVCFLPLHVLTVR 240
 Db 181 YLPLAVVVFCSLKVVTALAQRPTDVQQAETRAKRWANLIVFVVCFLPLHVLTVR 240
 QY 241 LAVGWNA CALLETIRRALYITSKLSANDCCCLDAICYYYMAKEFOEASALAVAPRAKAHS 300
 Db 241 LAVGWNA CALLETIRRALYITSKLSANDCCCLDAICYYYMAKEFOEASALAVAPRAKAHS 300
 QY 301 QDSLVCVTLA 309
 Db 301 QDSLVCVTLA 309
 RESULT 14
 ADA84069
 ID ADA84069 standard; protein; 309 AA.
 XX
 XX ADA84069;
 XX
 XX 20-NOV-2003 (first entry)
 XX
 XX Human GPR35 protein.
 XX
 XX human; marker; expressed sequence tag; EST; arabidopsis; tumour;
 XX stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
 XX vaccine.
 XX
 XX Homo sapiens.
 XX
 XX OS
 XX WO2002103028-A2.
 XX
 XX 27-DEC-2002.
 XX
 XX 30-MAY-2002; 2002WO-IB004189.
 XX
 XX 30-MAY-2001; 2001US-0293999P.
 XX
 XX 22-OCT-2001; 2001US-0330457P.
 XX
 XX 19-FEB-2002; 2002US-0357144P.
 XX
 XX (BIOM-) BIOMEDICAL CENT.
 XX
 XX Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;
 XX WPI; 2003-175241/17.
 XX
 XX N-PSDB; ADA84068.
 XX

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OM protein - protein search, using sw model

Run on: February 9, 2006, 01:00:39 : Search time 33.5 Seconds
(without alignments)
762.591 Million cell updates/sec

Title: US-10-083-168-16
Perfect score: 1614
Sequence: 1 MNGYNTCGSSDLTPPAIK.....AVAPRAKHSQDSLCVTLA 309

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6 COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1614	100.0	309	2	US-09-422-869-20
2	402	24.9	370	2	US-08-781-250-2
3	381.5	23.6	363	2	US-10-314-048A-159
4	375.5	23.3	363	2	US-10-314-048A-36
5	368.5	22.8	387	2	US-09-170-496D-108
6	368.5	22.8	387	2	US-09-170-496D-222
7	368.5	22.8	387	2	US-09-944-807-21
8	368.5	22.8	387	2	US-10-314-048A-135
9	362	22.4	372	2	US-09-875-076-4
10	361.5	22.4	344	1	US-08-467-947A-8
11	361.5	22.4	344	2	US-08-467-947A-8
12	360.5	22.3	302	1	US-08-467-948A-30
13	360.5	22.3	302	2	US-08-467-947A-30
14	348.5	21.6	360	2	US-10-314-048A-137
15	341.5	21.2	351	2	US-10-314-048A-157
16	341	21.1	361	2	US-10-314-048A-139
17	334.5	20.7	254	2	US-09-964-956-83
18	330.5	20.5	377	2	US-09-745-842-17
19	329.5	20.4	374	2	US-09-102-710B-3
20	327	20.3	346	2	US-10-314-048A-24
21	322.5	20.0	345	2	US-09-979-603-18
22	321	19.9	362	2	US-08-513-974B-374
23	320.5	19.9	343	2	US-10-314-048A-151
24	319.5	19.8	346	2	US-09-585-876-2
25	318	19.7	374	2	US-09-745-842-15
26	317.5	19.7	346	2	US-09-979-603-2
27	317.5	19.7	346	2	US-10-314-048A-14

28	317.5	19.7	346	2	US-10-314-048A-88	Sequence 88, Appl
29	317	19.6	309	2	US-09-979-603-22	Sequence 22, Appl
30	317	19.6	373	2	US-08-513-974B-373	Sequence 373, App
31	315.5	19.5	365	2	US-09-745-842-16	Sequence 16, Appl
32	315.5	19.5	365	2	US-09-077-173D-2	Sequence 2, Appl
33	312.5	19.4	364	2	US-08-148-708-2	Sequence 2, Appl
34	311.5	19.3	391	2	US-09-826-509-463	Sequence 463, App
35	310.5	19.2	327	2	US-08-513-974B-372	Sequence 372, App
36	310.5	19.2	362	2	US-09-170-496D-166	Sequence 166, App
37	310	19.2	342	2	US-08-988-876-9	Sequence 9, Appl
38	308.5	19.1	375	1	US-08-442-134A-2	Sequence 2, Appl
39	308.5	19.1	375	1	US-08-444-581B-2	Sequence 2, Appl
40	308.5	19.1	375	1	US-08-446-088A-2	Sequence 2, Appl
41	308.5	19.1	375	1	US-08-559-524A-3	Sequence 3, Appl
42	308.5	19.1	375	2	US-08-749-707-3	Sequence 3, Appl
43	308.5	19.1	375	2	US-09-947-922-3	Sequence 3, Appl
44	306	19.0	328	2	US-08-513-974B-39	Sequence 39, Appl
45	306	19.0	328	2	US-08-513-974B-371	Sequence 371, App

ALIGNMENTS

RESULT 1
US-09-422-869-20
; Sequence 20, Application US/09422869
; Patent No. 6235481
; GENERAL INFORMATION:
; APPLICANT: POLONSKY, KENNETH S.
; APPLICANT: HORIKAWA, YUKIO
; APPLICANT: ODA, NAOHISA
; APPLICANT: COX, NANCY J.
; APPLICANT: SREENAN, SEAMUS
; APPLICANT: ZHOU, YUN-PING
; APPLICANT: OTANI, KENICHI
; APPLICANT: HANIS, CRAIG L.
; APPLICANT: BELL, GRAEME I.
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
; FILE REFERENCE: ARCD:307
; CURRENT APPLICATION NUMBER: US/09/422,869
; CURRENT FILING DATE: 1999-10-21
; EARLIER APPLICATION NUMBER: 60/134,175
; EARLIER FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 20
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Human
US-09-422-869-20

Query Match	100.0%	Score 1614;	DB 2;	Length 309;
Best Local Similarity	100.0%;	Pred. No. 1.1e-129;		
Matches 309;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNGYNTCGSSDLTPPAIKLGFAYLGVLLVGLLNSLALWVFCRMOQTETRIYMT	60	
Db	1	MNGYNTCGSSDLTPPAIKLGFAYLGVLLVGLLNSLALWVFCRMOQTETRIYMT	60	
QY	61	NLAVALDCLLCTLPFVHSLRDTSTPLCSQGLYLTNRNYSISLVTAIADRVAVVRH	120	
Db	61	NLAVALDCLLCTLPFVHSLRDTSTPLCSQGLYLTNRNYSISLVTAIADRVAVVRH	120	
QY	121	PLRAGRLSPROAAACAVLWLVIGSLVARWLGIQEGGFCFRSTRHNFNMRPPLGFG	180	
Db	121	PLRAGRLSPROAAACAVLWLVIGSLVARWLGIQEGGFCFRSTRHNFNMRPPLGFG	180	
QY	181	YLPLAVVFCSLKVVYALAQRPPTDVGOAETRKAARVMWNLVVFVVCFLPLHVLTVR	240	
Db	181	YLPLAVVFCSLKVVYALAQRPPTDVGOAETRKAARVMWNLVVFVVCFLPLHVLTVR	240	
QY	241	LAVGNACALLETIRALYITSKLSDANCCLDIAICVYTMKEFOASALAVAPRAKHS	300	

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Db      241 LAVGNACALLETIRRALYITSKUSDANCCLDACYYMAKEPQESALAVAPRAKAKHS 300

QY      301 QDSLCVTLA 309
        |||||||
Db      301 QDSLCVTLA 309

RESULT 2
US-08-781-250-2
; Sequence 2, Application US/08781250
; Patent No. 6010877
; GENERAL INFORMATION:
; APPLICANT: Sathé, Ganesh
; APPLICANT: Van Horn, Stephanie
; APPLICANT: Bergama, Derk
; APPLICANT: Mao, Joyce Yue
; TITLE OF INVENTION: CDNA CLONE HE8CS41 THAT ENCODES A NOVEL 7-TRANSMEMBRAN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,250
; FILING DATE: 10-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han,
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4060
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-250-2

Query Match      24.9%; Score 402; DB 2; Length 370;
Best Local Similarity 34.1%; Pred. No. 1.6e-26;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY      25 AYLGVLLVGLLLNSLAWVCCRMQOWTETRYMNLAVADLCLLCTLPF-VLHSLR-- 81
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      44 AVYSVVFPLGLITNSVSLFVFCFMRKMRSETAIFITNLAVSDLLFVCTLPFKIFYNR 103
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      82 -DTSDTPLCOLSQGIYLTNEYMSISLVTAADVRYAVRHPLRARCLSPROAAAVCAVL 140
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      104 WPFGBT-LCKISGAFATNITYGSMFLTCISVDRLFAIVYFPRSRITRRNSAIVCAGV 162
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      141 WVLVIGSLVARWLLGIQK-----GGCFSTRHNFNSMR--FPLIGFYLPPLAVVVF 189
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      163 WILVLSGGISASLFSTIVNANNATTCPEGSKRVKWKYLSKITIFEVVGFIIPLINVS 222

QY      190 CSLKVVTAALQRPPTDVQGEAT-RKAARMVMWANLLVFVVCFLPLHVLGLTVRLAVGNAC 248
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      223 CSVVLRATL--RKPATLSQIGTKNKVKYLMITVHMAVFVVCVFPVNSVLFYALVRSQAI 280
        : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Qy 249 --ALLETIRALY-ITSKLSDANCCLDAICYYYWAKFQEQASALAVAPRAKAHKSQDSLC 305
Db 281 TNCPLERFAKIMYPITLCLATINCCFPDPFIYYFTLSEFQKSYI-----NAHIRMESLUF 334
Qy 306 VT 307
Db 335 KT 336

RESULT 3
US-10-314-048A-159
; Sequence 159, Application US/10314048A
; Patent No. 6902902
; GENERAL INFORMATION:
; APPLICANT: Unett, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Huong T.
; APPLICANT: Choi, Bryan
; APPLICANT: Leonard, James
; APPLICANT: Hakak, Yaron
; APPLICANT: Liaw, Chen
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lerner, Michael
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; FILE REFERENCE: 22 US6 CIP
; CURRENT APPLICATION NUMBER: US/10/314,048A
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096,511
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/995,543
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/399,917
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/404,761
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/410,747
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 159
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-048A-159

Query Match 23.6%; Score 381.5; DB 2; Length 363;
Best Local Similarity 34.2%; Pred. No. 8.5e-25;
Matches 94; Conservative 48; Mismatches 108; Indels 25; Gaps 9

Qy 27 LGVLLVLGLLNSIALWVFCRQOWTETRIYMTNLAVADCLICTIPFVLHSLRDSIT 86
Db 34 LGLEFIPGLGNGLAWIFCFHLKWSKSRIFLNLAVADFLLIICLPFLMDNIVRRSDW 93
Qy 87 PL-----QLSQSGYLTNRNYSISLVTAIAVDYVAVRHLRARGLRSPQAAAACAVLWV 142
Db 94 KFGDIPCLRLMLFPLAWNRRQSIIFLTVAVDYRVRVPHHALNKISNRTAAIISCLLWG 153
Qy 143 LVITGSLV--ARWLIGIQEGG--FCFR-STRHNP--NSMRPPLGLGFYLLPLAVVFCSLKVV 195
Db 154 ITIGLTVHLKKKMPIONGGANLCSFPSICHTFQWHEAMP-LLEFFFLPLGIILFCSARII 212
Qy 196 TALAQRPTDVQAEATRKAARWVANLLYVVCFLPLHVGLTVRLAVGW-----NAC 248
Db 213 WSLRQR---QMDRHAKIKRAITIMVVAIVFVICFLP---SVVVRIRIFMLLHSTGTQC 266
Qy 249 ALLETIRALYITSKLSDANCCLDAICYYYWAKF 283

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Db 267 EVYRSVDLAFITLSTFTYNSMLDPVYVYFSSPSF 301

RESULT 4

US-10-314-048A-36
; Sequence 36, Application US/10314048A

; Patent No. 6902902

; GENERAL INFORMATION:

; APPLICANT: Unett, David J.

; APPLICANT: Chen, Ruoping

; APPLICANT: Richman, Jeremy

; APPLICANT: Connolly, Daniel

; APPLICANT: Dang, Huang T.

; APPLICANT: Choi, Bryan

; APPLICANT: Leonard, James

; APPLICANT: Hakak, Yaron

; APPLICANT: Liaw, Chen

; APPLICANT: Lowitz, Kevin P.

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Lerner, Michael

; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof

; FILE REFERENCE: For the Treatment of Metabolic-Related Disorders

; CURRENT APPLICATION NUMBER: US/10/314,048A

; CURRENT FILING DATE: 2002-12-06

; PRIOR APPLICATION NUMBER: 10/096,511

; PRIOR FILING DATE: 2002-03-12

; PRIOR APPLICATION NUMBER: 09/995,543

; PRIOR FILING DATE: 2001-11-27

; PRIOR APPLICATION NUMBER: 60/399,917

; PRIOR FILING DATE: 2002-07-29

; PRIOR APPLICATION NUMBER: 60/404,761

; PRIOR FILING DATE: 2002-08-19

; PRIOR APPLICATION NUMBER: 60/410,747

; PRIOR FILING DATE: 2002-09-13

; NUMBER OF SEQ ID NOS: 161

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 36:

; LENGTH: 363

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-314-048A-36

Query Match 23.3%; Score 375.5; DB 2; Length 363;

Best Local Similarity 34.1%; Pred. No. 2.8e-24;

Matches 94; Conservative 48; Mismatches 107; Indels 27; Gaps 10;

QY 27 LGVLLVLGLLNSLALWVFCRCMQOWTETRIYMTNLAVADLCCLCTLPFVLHSL-----R 81

Db 34 LGLEFIFGLLGNGLALWIFCFHLKSKSRIFLFLNLAVADFLIICLPFLMDNYVRRWDW 93

QY 82 DTSPTPLCQLSQGIYLTNRYMSISLVTATAVDYVAVRHPLRARGLSRPRQAAVCAVLW 141

Db 94 KEGDIP-CRLVLFWMNRQSGIIFLTVAVDYVAVRHPLRARGLSRPRQAAVCAVLW 152

QY 142 VLVIGSLV--ARWLGIQGG--FCFR-STRNFP--NSMRPFLGFLPLAVVVCSLKV 194

Db 153 GITVGLTVHLKCKLL-IQNGPANVCISFISCHTFRHEAMF-LLEFPLPLGILFCSARI 211

QY 195 VTALAQRPTDVGQAEATKAARWYWANLLVFVCFPLPLHGLTVRLAVGW-----NA 247

Db 212 IWSLRQ---QMDRHAKIKRAITFMVVAIVFVICFLP---SVVVRIRFWLLHSTGTON 265

QY 248 CALLETIRRALYITSKLSANCCDAICYYYMAKEF 283

Db 266 CEVYRSVDLAFITLSTFTYNSMLDPVYVYFSSPSF 301

RESULT 5

US-09-170-496D-108

; Sequence 108, Application US/09170496D

; Patent No. 6555339

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: AREN-0040

; CURRENT APPLICATION NUMBER: US/09/170,496D

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 294

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 108

; LENGTH: 387

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-170-496D-108

Query Match 22.8%; Score 368.5; DB 2; Length 387;

Best Local Similarity 34.3%; Pred. No. 1.2e-23;

Matches 95; Conservative 48; Mismatches 105; Indels 29; Gaps 11;

QY 27 LGVLLVLGLLNSLALWVFCRCMQOWTETRIYMTNLAVADLCCLCTLPFVL-----HSLR 81

Db 34 LGLEFIFGLLGNGLALWIFCFHLKSKSRIFLFLNLAVADFLIICLPFVMDYVRRSDW 93

QY 82 DTSPTPLCQLSQGIYLTNRYMSISLVTATAVDYVAVRHPLRARGLSRPRQAAVCAVLW 141

Db 94 NFGDIP-CRLVLFWMNRQSGIIFLTVAVDYVAVRHPLRARGLSRPRQAAVCAVLW 152

QY 142 VLVIG---SLVARWLLGIQEG--GFCFR-STRNFP--NSMRPFLGFLPLAVVVCFLK 193

Db 153 GITVGLTVHLKCKLL-IQNGPANVCISFISCHTFRHEAMF-LLEFPLPLGILFCSAR 210

QY 194 VTALAQRPTDVGQAEATKAARWYWANLLVFVCFPLPLHGLTVRLAVGW-----N 246

Db 211 IWSLRQ---QMDRHAKIKRAITFMVVAIVFVICFLP---SVVVRIRFWLLHSTGTO 264

QY 247 ACALLETIRRALYITSKLSANCCDAICYYYMAKEF 283

Db 265 NCEVYRSVDLAFITLSTFTYNSMLDPVYVYFSSPSF 301

RESULT 6

US-09-170-496D-222

; Sequence 222, Application US/09170496D

; Patent No. 6555339

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: AREN-0040

; CURRENT APPLICATION NUMBER: US/09/170,496D

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 294

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 222

; LENGTH: 387

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-170-496D-222

Query Match 22.8%; Score 368.5; DB 2; Length 387;

Best Local Similarity 34.1%; Pred. No. 1.2e-23;

Matches 94; Conservative 47; Mismatches 108; Indels 27; Gaps 10;

QY 27 LGVLLVLGLLNSLALWVFCRCMQOWTETRIYMTNLAVADLCCLCTLPFVLHSLRSDT 86

Db 34 LGLEFIFGLLGNGLALWIFCFHLKSKSRIFLFLNLAVADFLIICLPFVMDYVRRSDW 93

QY 87 PL-----CQLSQGIYLTNRYMSISLVTATAVDYVAVRHPLRARGLSRPRQAAVCAVLW 142


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; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-875-076-4

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Query Match      22.4%; Score 362; DB 2; Length 372;
Best Local Similarity 33.7%; Pred. No. 4e-23;
Matches 109; Conservative 47; Mismatches 125; Indels 42; Gaps 12;

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DB      6 SSTSSVLPDYPYRTHRLHVVY-SLVLAAGLPLNALWVFLRALRVHSVVMCNL 64

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DB      179 FSDLMKGRLLPLVLAALGFLPLAAVVSGRVFWTLA-RP--DATQSORRRKTVRL 235

QY      219 VVANLLVVFVCPPLHVGTV-----PLAVGNACALLETIRRALYITSKLSANCCCLDAI 274
DB      236 LLANLVIFLLCFVPYNSTLAVVGLRSLKLVAAVSPARDVRGVLMVWLLAGANCVLDEL 295

QY      275 CYTYMAKEFOEA-SALAVAPRAK 296
DB      296 VTFFSAEGFRNLRGLGTHRAR 318

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RESULT 10
US-08-467-948A-8
; Sequence 8, Application US/08467948A
; Patent No. 5998164
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BULT, CAROL J.
; APPLICANT: SUTTON III, GRANGER G.
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
; TITLE OF INVENTION: Coupled Receptor GPR2
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,948A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04079
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-948A-8

Query Match      22.4%; Score 361.5; DB 1; Length 344;
Best Local Similarity 29.2%; Pred. No. 4e-23;
Matches 90; Conservative 68; Mismatches 107; Indels 43; Gaps 10;

QY      10 SSDLTWPPAIKLGFFAYL-GVLLVGLLNSLALWVFCRMOQWTTETRIYMTNLAVADLC 68
DB      6 SHCFYNDSFKTLGCMFSVVFVGLISNCVAIFICVLKVRNETTYTMINLMSDLL 65

QY      69 LLCTLPFLVHSLRDTSDTP---LCQLSQGIYLTNRVMSISLVAIAVDYVAVRHPLRA 124
DB      66 FVFTLPFRIFYF-TTRNWPFGDLLCKISVLMFYTNMYGSLFLTCTISVDRFLAIVVFPKS 124

QY      125 RGLRSPQAAVCAVLWLVV-GSLVARWLLIGIQEG-----FCFRSTRHNFSNMRFP-- 176
DB      125 KTLRTKRNKAVICTGVWLVTVIGSSAPAVFVQSTHSGQNNASACFEN-----FPEA 175

QY      177 -----LIGFVPLAVVVFCSLKVVTALAAORPPTDVGQAEATR-KAARMVWA 221
DB      176 TWKTYLSRIVIFIEIVGFPIPLILNVTCSMWLKITLK--PVTLSRSKINKYKLVKMFV 233

QY      222 NLLVVFVVCFLPHVGLTVRLAVGNWA---CALLETIRRALYITSKLSANCCCLDAICY 278
DB      234 HLIIFCFCFVPYNINILYSLVTRQTFVNCVVAARVWYPTITLCIAVSNCCFDPVIVVF 293

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QY 292 AP-----RAVAHKSOD-----SLC 305
Db 306 KPRRPGSRARRESEMPISNLC 327
Search completed: February 9, 2006, 01:02:27
Job time : 34.5 secs

Db 210 WSLRQR---QMDRHAKIKRAINFMVVAIFICFLP---SVAVRIRIFWLLKYKYNVNC 263
QY 249 ALLETIRRALYITSKJSDANCCCLDAICYYYMAKEF 283
Db 264 DIYSSVDLAFFTLSTFTYMSMLDPVVYYFSPSF 298

RESULT 15

US-10-314-048A-157
; Sequence 157, Application US/10314048A
; Patent No. 6902902
; GENERAL INFORMATION:
; APPLICANT: Unsett, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Huong T.
; APPLICANT: Choi, Bryan
; APPLICANT: Leonard, James
; APPLICANT: Hakak, Yaron
; APPLICANT: Liaw, Chen
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lerner, Michael
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; FILE REFERENCE: 22.US6.CIP
; CURRENT APPLICATION NUMBER: US/10/314,048A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096,511
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/995,543
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/399,917
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/404,761
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/410,747
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 157
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Rat
US-10-314-048A-157

Query Match 21.2%; Score 341.5; DB 2; Length 351;
Best Local Similarity 33.2%; Pred. No. 2.1e-21;
Matches 107; Conservative 48; Mismatches 114; Indels 53; Gaps 15;
QY 16 PPAIKGFGYALGVLLVIGLLNSLAWVFCRQWQWETRIYMTNLAVADLCLCTLPF 75
Db 27 PPLILAF-----LLGALGNGLACGCFHMKTKWKSSTIYFLNLAADVFLMLCLPL 78
QY 76 -VLHSLRD---TSDTPLCQSQIYLTNRYMSISLVTAIAVDYVAVRHPLRARGLRSP 130
Db 79 RTDYLLRRRHILGDIP-CLRLVFLMLAMNRAGSIVFTVAVDRYFKVVPHPHMVNAISN 137
QY 131 RQAAVCAVLWLVIGSLVARWILGIGQGGCFPR-----STRHFNFSNRPPLLG 179
Db 138 RTAAAIVCVLTWLVILGTV--YLL--MESHLCVRGMVSSCESFTMESANGWHDIMFQ-LE 192
QY 180 FYLPLAVVVFCSLKVYALAQRPPTDVQAEATKAAKRWYMANLLVPVVCFLPHVGLTV 239
Db 193 FFLPLTILFCSPKVVWSLRQR--QQLTRQARMRRATRFIMVASVFITCYLP---SVLA 247
QY 240 RLAVGW---NACALLETIRRALYITSKJSDANCCCLDAICYYYMAKEFQEASA-----LAV 291
Db 248 RLYFLWTVPSACD--PSVHIALHVTLSLYVLSNMLDPLVYFSPSPFPKFKYAKLIRSL 305

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 02:58:32 ; Search time 5114 Seconds
(without alignments)
10337.194 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb.env.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pr.*
9: gb.ro.*
10: gb.sts.*
11: gb.sy.*
12: gb.un.*
13: gb.vi.*
14: gb.htg.*
15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	925.2	99.5	930	CS122237	Sequence
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3	925.2	99.5	1299	AF027957	Homo sapi
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5	922	99.1	169391	AC111190	Homo sapi
6	920.4	99.0	930	AY275467	Homo sapi
7	920.4	99.0	930	CR541765	Homo sapi
8	920.4	99.0	930	AY893518	Synthetic
9	920.4	99.0	1875	AR153299	Sequence
10	920.4	99.0	1875	Q0821493	Sequence
11	920.4	99.0	1875	AX677157	Sequence
12	920.4	99.0	1875	AF089087	Homo sapi
13	920.4	99.0	49136	AR153289	Sequence
14	920.4	99.0	65674	AF158748	Homo sapi
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19	914.8	98.4	926	8	BC095500	Homo sapi
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21	549.2	59.1	2508	8	AB041940	Homo sapi
22	549.2	59.1	2538	9	BC027429	Mus muscu
23	549.2	59.1	2582	9	AF200349	Mus muscu
c 24	549.2	59.1	209326	9	AC110247	Mus muscu
c 25	549.2	59.1	242338	9	AC119846	Mus muscu
26	546	58.7	220053	14	AC137209	Rattus no
27	514.2	55.3	599	6	CQ920514	Sequence
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33	111.2	12.0	1089	11	AY893725	Synthetic
c 34	111.2	12.0	1268	8	BC095534	Homo sapi
35	111.2	12.0	1365	6	AR270866	Sequence
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45	110.4	11.9	960	6	CQ737276	Sequence

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LOCUS CS122237 930 bp DNA linear PAT 16-JUL-2005
DEFINITION Sequence 1 from Patent WO2005059546.
ACCESSION CS122237
VERSION CS122237.1 GI:70911057
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Golz, S.
TITLE Diagnostics and therapeutics for diseases associated with g
protein-coupled receptor 35 (gpr35)
JOURNAL Patent: WO 2005059546-A 1 30-JUN-2005;
Bayer HealthCare AG (DE)
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source Location/Qualifiers
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/mol_type="unassigned DNA"
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61	CTGGGGCTTCTACGCCCTACTTGGGCGTCTGTGGTGTCTAGGCTGTCTCAACAGCCTG								
61	CTGGGGCTTCTACGCCCTACTTGGGCGTCTGTGGTGTCTAGGCTGTCTCAACAGCCTG								
121	GGCTCTGGGTTCTTCTGTCTGGCGGATGCGAGTGGACCGGACCGGATCTACATGACC								
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[illegible]

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Dd	514	TACATGAGCATCAGCTGTGTACGGCCATCGCGTGGACCGCTATGTGCGCTGCGGCAC	573
Qy	361	CCGCTCGTGCCCGCGGGCTGCGGTCCCCAGCAGGCTGCGGCCGTGTGCGGGTCCTC	420
Dd	574	CCGCTCGTGCCCGCGGGCTGCGGTCCCCAGCAGGCTGCGGCCGTGTGCGGGTCCTC	633
Qy	421	TGGGTGTGTGTCAATCGGCTCCCTGTGTGTGCTGCTTCTTGGGGATTACAGAGGGCGCG	480
Dd	634	TGGGTGTGTGTCAATCGGCTCCCTGTGTGTGCTGCTTCTTGGGGATTACAGAGGGCGCG	693
Qy	481	TTCTGTCTTCAGGAGCACCCGGGCACAATTTCAAATCTCATGCGGTTCGCGTGTGCGGATTC	540
Dd	694	TTCTGTCTTCAGGAGCACCCGGGCACAATTTCAAATCTCATGCGGTTCGCGTGTGCGGATTC	753
Qy	541	TACTGCGCCCTGCGCCGTGTGTGTCTTCTGTCTCCCTGAAGGTGTGTGACTGCGCTTGGCCCAG	600
Dd	754	TACTGCGCCCTGCGCCGTGTGTGTCTTCTGTCTCCCTGAAGGTGTGTGACTGCGCTTGGCCCAG	813
Qy	601	AGGCCACCCACCGACGTGGGGCAGGAGGCCAACCCGCAAGGCTAAACGATGTGTCTGG	660
Dd	814	AGGCCACCCACCGACGTGGGGCAGGAGGCCAACCCGCAAGGCTAAACGATGTGTCTGG	873
Qy	661	GCCAACTCTCTGTGTGTGTGTGTCTTCTTCTGCTGCACTGCGGGCTGCACAGTGC	720
Dd	874	GCCAACTCTCTGTGTGTGTGTGTCTTCTTCTGCTGCACTGCGGGCTGCACAGTGC	933
Qy	721	CTGCGCTGGGCTGGAACGCTGTGCGCCCTCTTGAGACGATCCGTGCGGCCCTGTATACATA	780
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Qy	781	ACCAGCAAGCTCTCAGATGCACTGTGCTGTGAGGCCCATCTGCTACTACTACTATGCGCC	840
Dd	994	ACCAGCAAGCTCTCAGATGCACTGTGCTGTGAGGCCCATCTGCTACTACTACTATGCGCC	1053
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Dd	1114	CAGGACTCTCTGTGCGTGACCTCGCCCTAA	1143
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AKI72786			
LOCUS	Homo sapiens cDNA FLJ23947 fis, clone HEP05863, highly similar to G	2270 bp	mRNA linear PRI 07-MAY-2004
DEFINITION	protein-coupled receptor GPR35.		
ACCESSION	AKI72786		
VERSION	AKI72786.1 GI:47077780		
KEYWORDS	oligo capping; his (full insert sequence).		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homindae; Homo.		
REFERENCE	1		
AUTHORS	Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Maesumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Oca,T., Suzuki,Y., Obayashi,M., Nishi.T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEDO human cDNA sequencing project Unpublished 2 (bases 1 to 2270) Sugano,S. and Suzuki,Y. Direct Submission Submitted (22-APR-2004) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shiokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: flicdn@mail.ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)		
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library insert construction; 5'- & 3'-end one pass sequencing; Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

FEATURES Location/Qualifiers

source 1. .2270 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="HEP05863" /cell_line="HepG2" /cell_type="hepatoma" /clone_lib="HEP" /note="cloning vector pME18SFL3"

ORIGIN

Query Match 99.1%; Score 922; DB 8; Length 2270; Best Local Similarity 99.5%; Pred. No. 2.4e-120; Mismatches 5; Indels 0; Gaps 0; Matches 925; Conservative 0;

Qy 1 ATGAATGGCACTACACACCTGTGGCTCCAGGACCTACCTGTGGCCCCCAGGATCAAG 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 943 ATGAATGGCACTACACACCTGTGGCTCCAGGACCTACCTGTGGCCCCCAGGATCAAG 1002
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Qy 1003 CTGGGCTTCTACGGCTACTTGGGGTCTCTGGTGTAGGCTGTGCTCAACAGGCTG 1062
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Qy 1063 GCCTCTGGGTGTCTGCTCCGATGACAGTGGAGGAGACCCGCACTCATAGTACC 1122
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 181 AACCTGGCGTGGCCGACCTCTGCTGTGTGACCTTGGCCCTTCTGTGCTGCACTCCCTG 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Qy 361 CGCTGTGCTGCCGCGGCTGTGCTGCCAGGAGCTGTGCGGCTGTGCGGCTGTGCTC 420
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LOCUS
DEFINITION Homo sapiens chromosome 2 clone RPI3-511H14, WORKING DRAFT
SEQUENCE 7 unordered pieces.
AC111190
VERSION AC111190.2 GI:21426750
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 169391)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 169391)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (18-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 3 (bases 1 to 169391)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jun 14, 2002 this sequence version replaced gi:18699976.
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.edu
----- Project Information -----
Center project name: H.FH0511H14
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Assembly: Dye-terminator Big Dye; 100% of reads
Consensus quality: 167477 bases at least Q40
Consensus quality: 168018 bases at least Q30
Consensus quality: 168194 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 168791; sum-of-contigs
Quality coverage: 9.18 in Q20 bases; agarose-fp
Quality coverage: 9.60 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence

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Best Local Similarity 99.4%; Pred. No. 4.9e-120;
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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DB |
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DB |
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DB |
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841 AAGGAGTTCCAGGAGCGCTGTGCACTGGCCGCTGCTCCAGTGCTTAAGGCCCAAAAAGC 900

901 CAGGACTCTCTGTGCTGCTGACCTCCCTAA 930

901 CAGGACTCTCTGTGCTGCTGACCTCCCTAA 930

RESULT 7

CR541765 930 bp mRNA linear PRI 29-JUN-2004

Homo sapiens full open reading frame cDNA clone RZPD0834D0330D for gene GPR35, G protein-coupled receptor 35; complete cds, incl. stopcodon.

CR541765

CR541765.1 GI:49456486

Full ORF shuttle clone, Gateway(TM), complete cds.

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 930)

Halleck,A., Ebert,L., Moundinya,M., Schick,M., Eisenstein,S., Neubert,P., Katrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.

Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)

Unpublished

2 (bases 1 to 930)

Halleck,A., Ebert,L., Moundinya,M., Schick,M., Eisenstein,S., Neubert,P., Katrang,K., Schatten,R., Shen,B., Henze,S., Mar,W., Korn,B., Zuo,D., Hu,Y. and LaBaer,J.

Direct Submission

Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

COMMENT

RZPD: RZPD0834D0330D, ORFNO 3528

www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD0834D0330D RZPDLIB; Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No. 834

www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834

www.rzpd.de/products/orfclones/

Contact: Inge Ariart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 100

Fax: +49 30 32639 111

www.rzpd.de

This clone is available from RZPD;

Contact RZPD (customer.service@rzpd.de) for further information.

Clone name at Harvard Institute of Proteomics (www.hip.harvard.edu): FLH13100.01X

This CDS clone is part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD.

This CDS has been cloned incl. stopcodon.

The CDS has been inserted into pDONR201 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the start codon: att..AAAAA GCA GGC TCC ACC (ATG).

The stopcodon is followed by the 3' att site: GACCCAGCTTTCTT..att

The clone is validated by full sequence check.

Compared to the reference sequence NM_005301 (GI:33695096) we found

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Clone distribution: http://www.rzpd.de/products/orfclones/.					
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ORIGIN					
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	Best Local Similarity	99.4%;	Pred. No. 4.9e-120;		
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Qy	1	ATGAATGGCACCTACAACACTGTGGCTCCAGCGACCTCACTCGCCCCCAGCGCATCAAG	60		
Dd	1	ATGAATGGCACCTACAACACTGTGGCTCCAGCGACCTCACTCGCCCCCAGCGCATCAAG	60		
Qy	61	CTGGGCTTTACGCCTACTTGGGGCGTCCTGCTGTGTCTAGGCCCTGCTCTCAACAGCGTG	120		
Dd	61	CTGGGCTTTACGCCTACTTGGGGCGTCCTGCTGTGTCTAGGCCCTGCTCTCAACAGCGTG	120		
Qy	121	GGCGTCTGGGGTGTCTGCTGCCGATGCAGCAGTGGAGCGGAGACC CGCATCTACATGACC	180		
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Dd	541	TACCTGGCCCTTGGCGGTGTGTCTTCTGCTCCCTGAAAGTGGTGACTGCGCTGGCCCGAC	600		
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DEFINITION Sequence 1 from Patent WO2004047863.
ACCESSION CQ821493
VERSION CQ821493.1 GI:49019245
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Sahin,U., Tuercel,O. and Koslowski,M.
Genetic products differentially expressed in tumors and the use
thereof
JOURNAL Patent: WO 2004047863-A 1 10-JUN-2004;
Ganymed Pharmaceuticals AG (DE)
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ORIGIN
Query Match 99.0%; Score 920.4; DB 6; Length 1875;
Best Local Similarity 99.4%; Pred. No. 4.2e-120;
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACTGGCCCCCAGCGATCAAG 60
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Db 1476 CAGGACTCTCTGTGCTGACCTCGCCTAA 1505

RESULT 11
AX677157
LOCUS AX677157 1875 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 350 from Patent WO02103028.
ACCESSION AX677157
VERSION AX677157.1 GI:29334605
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Baranova,A.V., Yankovsky,N.K., Kozlov,A.P., Lobashev,A.V. and
Krukovskaya,L.I.
In silico screening for phenotype-associated expressed sequences
JOURNAL Patent: WO 02103028-A 350 27-DEC-2002;
Biomedical Center (RU)
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ORIGIN
Query Match 99.0%; Score 920.4; DB 6; Length 1875;
Best Local Similarity 99.4%; Pred. No. 4.2e-120;
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACTGGCCCCCAGCGATCAAG 60
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Db      636 CTGGGCTTCTACGCTTACTTGGGGTCTCTGTGGTGTAGGCTGTGCTCAACAGCCTG 695
Qy      121 GCCTCTGGGTGTCTGCTCGCGATGACAGTGTGAGGAGACCCGCTACTACATGACC 180
Db      696 GCCTCTGGGTGTCTGCTCGCGATGACAGTGTGAGGAGACCCGCTACTACATGACC 755
Qy      181 AACCTGGCGTGGCCGACCTCTGCTGTGTGACCTTGGCCCTTGTGCTGCACTCCCTG 240
Db      756 AACCTGGCGTGGCCGACCTCTGCTGTGTGACCTTGGCCCTTGTGCTGCACTCCCTG 815
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Db      816 CGAGACACTCAGACAGCGCGTGTGCGAGCTTCCAGGGCATCTACCTGACCAACAGG 875
Qy      301 TACATGAGCATCAGCTGTGTCAGGCGCATCGCGTGGACCGCTATGTGGCGGTGGGCAC 360
Db      876 TACATGAGCATCAGCTGTGTCAGGCGCATCGCGTGGACCGCTATGTGGCGGTGGGCAC 935
Qy      361 CCCTGTGCTCGCGCGGCTGCGGTCCCGCAGGCGAGGCTCGCGCGGTGCGCGGCTCCTC 420
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LOCUS      AF089087
DEFINITION Homo sapiens G protein-coupled receptor mRNA, complete cds.
ACCESSION AF089087
VERSION    AF089087.1
KEYWORDS   GI:10503932
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 1875)
Horikawa,Y., Oda,N., Cox,N.J., Li,X., Orho-Melander,M., Hara,M.,
Hinokio,Y., Lindner,T.H., Mashima,H., Schwarz,P.E., del
Bosque-Plata,L., Horikawa,Y., Oda,Y., Yoshiuchi,I., Colilla,S.,
Polonsky,K.S., Wei,S., Concannon,P., Iwasaki,N., Schulse,J., and
Baier,L.J., Bogardus,C., Groop,L., Boerwinkle,E., Hanis,C.I. and
Bell,G.I.
Genetic variation in the gene encoding calpain-10 is associated
with type 2 diabetes mellitus
Nat. Genet. 26 (2), 163-175 (2000)
11017071
2 (bases 1 to 1875)
Horikawa,Y. and Bell,G.I.
Direct Submission
Submitted (02-SEP-1998) Howard Hughes Medical Institute, The
University of Chicago, 5841 S. Maryland Avenue, MC1028, Chicago, IL
60637, USA
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DEFINITION Sequence 1 from patent US 6235481.
ACCESSION AR153289
VERSION AR153289.1 GI:15120821
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 49136)
AUTHORS Horikawa,Y., Oda,N., Hanis,C.L., Bell,G.I. and Cox,N.J.
TITLE Polynucleotides encoding calpain 10
JOURNAL Patent: US 6235481-A 1 22-MAY-2001;
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Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DEFINITION Homo sapiens map 2q37.3, genomic sequence.
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VERSION AF158748.3 GI:20260805
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1 (bases 1 to 65674)
AUTHORS Horikawa,Y., Oda,N., Cox,N.J., Li,X., Orho-Melander,M., Hara,M.,
  Hinokio,Y., Lindner,T.H., Mashima,H., Schwarz,P., del Bosque
  Plata,L., Horikawa,Y., Oda,Y., Yoshiuchi,I., Colilla,S.,
  Polonsky,K.S., Wei,S., Concannon,P., Iwasaki,N., Schulze,J.,
  Baier,L.J., Bogardus,C., Groop,L., Boerwinkle,E., Hanis,C.L. and
  Bell,G.I.
TITLE Genetic variation in the gene encoding calpain-10 is associated
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AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Waterston, R.
 Direct Submission
 Submitted (15-Oct-2002) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 7 (bases 1 to 160111)
 Wilton, R.K.
 Direct Submission
 Submitted (15-APR-2005) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Sep 8, 2002 this sequence version replaced gi:22091410.

 Center: Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu>
 Contact: submissions@watson.wustl.edu

 Summary Statistics
 Center project name: H_NH0027M15
 Drafting Center: WBR

NOTICE:
 This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by
 restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. Wes Warren,
 Department of Genetics, Washington University, St. Louis MO. For
 additional information about the map position of this sequence, see
<http://genome.wustl.edu>

SOURCE INFORMATION:
 The RPCI-11 human BAC library was made from the blood of one male
 donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E.,
 Tatenio, M., Catanese, J.J. and de Jong, P.J. (1998) An improved
 approach for construction of bacterial artificial chromosome
 libraries. Genomics 51:1-8. The clone may be obtained either from
 Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong
 and coworkers at <http://www.choxi.org>
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
 This sequence is not the entire insert of the clone. This clone is
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The sequence of AC080022 has been incorporated into AC124862.

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Query Match 99.0%; Score 920.4; DB 8; Length 160111;		
Best Local Similarity 99.4%; Pred. No. 1.5e-120;		
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Search completed: February 11, 2006, 04:54:32
Job time : 5119 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 00:25:50 ; Search time 684 Seconds
(without alignments)
9061.643 Million cell updates/sec

Title: US-10-083-168-84
Perfect score: 930
Sequence: 1 atgaatggcaccatacaac.....tgtgctgaccctgcctaa 930

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 21.*

- 1: geneseqn1980s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002as.*
- 7: geneseqn2002bs.*
- 8: geneseqn2003as.*
- 9: geneseqn2003bs.*
- 10: geneseqn2003cs.*
- 11: geneseqn2003ds.*
- 12: geneseqn2004as.*
- 13: geneseqn2004bs.*
- 14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	930	100.0	930	6	ABST73401
2	925.2	99.5	930	6	ABST73401 DNA enco
3	925.2	99.5	930	6	ABST73401 DNA enco
4	925.2	99.5	930	9	ABST73401 DNA enco
5	925.2	99.5	930	12	ADQ29916 Human GPC
6	925.2	99.5	930	14	ADQ29916 Human GPC
7	925.2	99.5	930	14	ADQ29916 Human GPC
8	922	99.1	1369	3	AAZ50891 Human rec
9	920.4	99.0	1875	3	AAZ50891 Human rec
10	920.4	99.0	1875	3	AAZ50891 Human rec
11	920.4	99.0	1875	3	AAZ50891 Human rec
12	920.4	99.0	1875	3	AAZ50891 Human rec
13	919	98.8	1844	10	ADP70563 Orphan re
14	917.2	98.6	3811	13	ADP70563 Orphan re
15	915.6	98.5	1043	3	AAZ35390 Human G-p
16	900	96.8	1989	6	ABZ35525 Human gen
17	838	90.1	858	12	ADP28534 Human sec
18	549.2	59.1	924	12	ADQ30206 Mouse GPC
19	514.2	55.3	599	13	ADU11275 Solid tum

20	431.4	46.4	569	14	ACL58361	ACL58361 Human col
21	141.8	15.2	1854	4	AAI10133	AAI10133 Mouse G p
22	141.8	15.2	1854	6	ABL35067	ABL35067 Murine cD
23	120.6	13.0	121	10	ADP87215	ADP87215 Single nu
24	111.6	12.0	1098	3	AAA30740	AAA30740 DNA enco
25	111.6	12.0	1098	10	ADQ22744	ADQ22744 Human G p
26	111.6	12.0	1098	10	ADH14217	ADH14217 Mutated h
27	111.2	12.0	1089	3	AAA30581	AAA30581 Human G p
28	111.2	12.0	1089	6	AAZ26832	AAZ26832 Human G-p
29	111.2	12.0	1089	8	ACC78113	ACC78113 Human G p
30	111.2	12.0	1089	10	ADQ22522	ADQ22522 Human G p
31	111.2	12.0	1089	10	ADH13995	ADH13995 Human GPR
32	111.2	12.0	1089	12	ADQ29766	ADQ29766 Human nov
33	111.2	12.0	1365	6	ABZ34905	ABZ34905 Human gen
34	111.2	12.0	1365	10	ACA56831	ACA56831 Human sig
35	111.2	12.0	1365	12	ADJ56627	ADJ56627 Human pol
36	111.2	12.0	2693	8	AAZ50858	AAZ50858 Human G-p
37	111.2	12.0	2696	8	ABZ42741	ABZ42741 Human G p
38	111.2	12.0	2696	12	ADP17570	ADP17570 Human G p
39	111.2	12.0	2696	12	ADQ28684	ADQ28684 Human GPR
40	111.2	12.0	2696	12	ADQ28684	ADQ28684 Human GPR
41	111.2	12.0	2696	13	ADS75991	ADS75991 Human GPR
42	111.2	12.0	2932	6	AAZ26831	AAZ26831 Human G-p
43	111.2	12.0	2932	12	ADL71938	ADL71938 Human GPR
44	111.2	12.0	2932	13	ADS19844	ADS19844 Human GPR
45	111.2	12.0	2932	13	ADU06778	ADU06778 Human GPR

ALIGNMENTS

RESULT 1

ABST73401

ID ABST73401 standard; DNA; 930 BP.

AC ABST73401;

DT 04-DEC-2002 (first entry)

DE DNA encoding human GPCR GPR35 mutant A216K.

XX Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;
XX hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;
XX psychotic disorder; asthma; bronchospasm; anaesthesia;
XX myocardial infarction; MI; stroke; glaucoma; anxiety;
XX prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;
XX prostatic hypertrophy; mutant; ds.

OS Homo sapiens.

OS Synthetic.

XX WO200268600-A2.

PD 06-SEP-2002.

XX 26-FEB-2002; 2002WO-US005625.

XX 26-FEB-2001; 2001US-0271913P.

XX (AREN-) ARENA PHARM INC.

PI Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;
PI Lin I, Ortuno D;

DR WPI; 2002-706980/76.

XX P-PSDB; ABG95172.

PT New human G-protein coupled receptor (GPCR), useful for screening agonist
PT or inverse agonist compounds for treating diseases associated with GPCR.

XX Example 2; Page 188-189; 201pp; English.

XX The present invention relates to transmembrane receptors, particularly


```
Db 121 GCGCTCTGGGTCTCTGCTCCGATGACAGAGTGGAGCGAGACCGCATCTACATGACC 180
Qy 181 AACCTGGCGGTGGCGGACCTCTGCTGTCTGTGCACTTGGCCCTTGTGCTGCACTCCCTG 240
Db 181 AACCTGGCGGTGGCGGACCTCTGCTGTCTGTGCACTTGGCCCTTGTGCTGCACTCCCTG 240
Qy 241 CGAGACACCTCAGACAGCGCGCTGTGCCAGCTCTCCGAGGGCATCTACCTGACCAACAGG 300
Db 241 CGAGACACCTCAGACAGCGCGCTGTGCCAGCTCTCCGAGGGCATCTACCTGACCAACAGG 300
Qy 301 TACATGAGCATCAGCTGTGTGACGGCCATCGCGGTGGACCGCTATGTGGCGGTGCGGCAC 360
Db 301 TACATGAGCATCAGCTGTGTGACGGCCATCGCGGTGGACCGCTATGTGGCGGTGCGGCAC 360
Qy 361 CCGTGTGCTGCCGCGGCTGTGCCAGGAGGCTGTGCCGCGGTGTGCCGCGGTCTC 420
Db 361 CCGTGTGCTGCCGCGGCTGTGCCAGGAGGCTGTGCCGCGGTGTGCCGCGGTCTC 420
Qy 421 TGGGTGTGCTGTGCTGCTCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 TGGGTGTGCTGTGCTGCTCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 481 TTCTGCTTTCAGGACGACCCCGGCAAAATTTCAAATTCATGCGGTTCCTGCTGCTGCTG 540
Db 481 TTCTGCTTTCAGGACGACCCCGGCAAAATTTCAAATTCATGCGGTTCCTGCTGCTGCTG 540
Qy 541 TACTGTCCCTGTGCGGTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 TACTGTCCCTGTGCGGTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy 601 AGGCCACCCAGCAGTGGGGGAGGCGAGGCGCACCGCGGAGGCTAAACGATGCTGCTGG 660
Db 601 AGGCCACCCAGCAGTGGGGGAGGCGAGGCGCACCGCGGAGGCTGCGCGCATGCTGCTGG 660
Qy 661 GCCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 GCCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Qy 721 CTCGCAATGGGCTGGAACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 CTCGCAATGGGCTGGAACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Qy 781 ACCAGCAAGCTCTCAGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 781 ACCAGCAAGCTCTCAGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy 841 AAGGAGTTCAGAGGCGCTGCACTGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 AAGGAGTTCAGAGGCGCTGCACTGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Qy 901 CAGGACTCTCTGTGCGTGACCTTCGCTAA 930
Db 901 CAGGACTCTCTGTGCGTGACCTTCGCTAA 930
```

RESULT 4

ADB67672
ID ADB67672 standard; DNA; 930 BP.

AC ADB67672;

XX 04-DEC-2003 (first entry)

DE Human G protein-coupled receptor 35 DNA, SEQ ID 10.

XX Cardiant; Gene therapy; heart failure; gene; ds; human;

XX G protein-coupled receptor 35; receptor.

XX Homo sapiens.

XX WO2003072824-A1.

PD 04-SEP-2003.
XX 27-FEB-2003; 2003WO-JP002228.
XX 28-FEB-2002; 2002JP-00054388.
PR 15-APR-2002; 2002JP-00112228.
XX (SANY) SANKYO CO LTD.
XX Kitakaze M, Takashima S, Asakura M, Isomura T, Furukawa H;
PI Koishi R, Nakamaru K;
XX WPI: 2003-679959/64.
DR P-PSDB; ADB67656.
XX Predicting pathological conditions in heart failure using marker genes
and proteins.
PS Claim 1; Page 78; 137pp; Japanese.
XX The present invention relates to a method for predicting pathological
conditions in heart failure using expression of one of 17 gene sequences
(ADB67663-ADB67678); or protein sequences encoded by the genes (ADB67648-
ADB67662). The proteins and genes are useful for diagnosis, treatment and
prevention of heart failure.
SQ Sequence 930 BP; 138 A; 328 C; 279 G; 185 T; 0 U; 0 Other;

Query Match 99.5%; Score 925.2; DB 9; Length 930;

Best Local Similarity 99.7%; Pred. No. 1.9e-175;

Matches 927; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACCTGCCCCCAGCATCAAG 60

Db 1 ATGAATGGCACCTACAACACCTGTGGCTCCAGCGACCTCACCTGCCCCCAGCATCAAG 60

Qy 61 CTGGGCTTCTACGCTTACTTGGGCGTCTGCTGGTGTAGGCTGCTGCTCAACAGCCTG 120

Db 61 CTGGGCTTCTACGCTTACTTGGGCGTCTGCTGGTGTAGGCTGCTGCTCAACAGCCTG 120

Qy 121 GCGCTCTGGGTGTCTGCTGCCCATGACAGCAGTGGAGCGAGACCGCATCTACATGACC 180

Db 121 GCGCTCTGGGTGTCTGCTGCCCATGACAGCAGTGGAGCGAGACCGCATCTACATGACC 180

Qy 181 AACCTGGCGGTGGCGGACCTCTGCTGTGTGCACTTGTGCTGCTGCTGCTGCTGCTG 240

Db 181 AACCTGGCGGTGGCGGACCTCTGCTGTGTGCACTTGTGCTGCTGCTGCTGCTGCTG 240

Qy 241 CGAGACACCTCAGACAGCGCGCTGTGCCAGCTCTCCAGGGCATCTACCTGACCAACAGG 300

Db 241 CGAGACACCTCAGACAGCGCGCTGTGCCAGCTCTCCAGGGCATCTACCTGACCAACAGG 300

Qy 301 TACATGAGCATCAGCTGTGTGCAAGCGCATGCGCGGTGGACCGCATGTGCGCGGTGCGGCAC 360

Db 301 TACATGAGCATCAGCTGTGTGCAAGCGCATGCGCGGTGGACCGCATGTGCGCGGTGCGGCAC 360

Qy 361 CCGCTGCGTGGCGCGGCTGCGGCTGCCCGCAGCGAGGCTGCGGCGGTGCTGCTGCTGCTC 420

Db 361 CCGCTGCGTGGCGCGGCTGCGGCTGCCCGCAGCGAGGCTGCGGCGGTGCTGCTGCTGCTC 420

Qy 421 TGGGTGTGCTCATCGGCTCCCTGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

Db 421 TGGGTGTGCTCATCGGCTCCCTGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

Qy 481 TTCTGCTTCAGGAGCACCGCGCAAAATTTCAACTCCATGCGGTTCCTGCTGCTGCTGCTG 540

Db 481 TTCTGCTTCAGGAGCACCGCGCAAAATTTCAACTCCATGCGGTTCCTGCTGCTGCTGCTG 540

Qy 541 TACCTGCCCCCTGGCGGTGTGCTTCTGCTCCTGAAAGGTGTGCTGCTGCTGCTGCTGCTG 600

Db 541 TACCTGCCCCCTGGCGGTGTGCTTCTGCTCCTGAAAGGTGTGCTGCTGCTGCTGCTGCTG 600

Qy 601 AGGCCACCCAGCAGTGGGGGAGGCGGACCGCGCAGGCTTAAGCGCATGTGCTGCTGCTG 660

601	Db		AGGCCACCCAGCAGTGGGCGAGGAGGCGACCCCGCAGGCTGCCCGCATGCTGG	660
661	Qy		GCCAACTCTGGTGTTCGTGGTCTGCTCTCTGCCCCCTGCAGTGGGGCTGACAGTGGCG	720
661	Db		GCCAACTCTCTGGTGTTCGTGGTCTGCTCTCTGCCCCCTGCAGTGGGGCTGACAGTGGCG	720
721	Qy		CTCGCAGTGGGCTGGAACGCCCTGTGGCCCTCTCTGGAGAGCATCCGTGGCGCCCTGTACATA	780
721	Db		CTCGCAGTGGGCTGGAACGCCCTGTGGCCCTCTCTGGAGAGCATCCGTGGCGCCCTGTACATA	780
781	Qy		ACCGCAGGCTCTCAGATGCCAACTGCTGCCGTGGAGCGCATCTGCTACTACTACATGGCC	840
781	Db		ACCGCAGGCTCTCAGATGCCAACTGCTGCCGTGGAGCGCATCTGCTACTACTACATGGCC	840
841	Qy		AAGGAGTTCCAGGAGGCGCTCTGCATCTGGCCGCTGGGCTCCCGTCTAAGGCCCAAAAGC	900
841	Db		AAGGAGTTCCAGGAGGCGCTCTGCATCTGGCCGCTGGGCTCCCGTCTAAGGCCCAAAAGC	900
901	Qy		CAGGACTCTGTGGTGACCCCTGCGCTAA	930
901	Db		CAGGACTCTGTGGTGACCCCTGCGCTAA	930

RESULT 5
ADO29916
ID ADO29916 standard; cDNA; 930 BP.
XX
XX ADO29916;
XX AC
XX
XX
DT 29-JUL-2004 (first entry)
XX
XX
DE Human GPCR GPR35 polynucleotide. SEQ ID NO:1018.

G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; immune disorder; bone disorder; joint disorder; metabolic disorder; nutritive disorder; cancer; kidney disorder; liver disorder; lung disorder; breast disorder; ovary disorder; uterus disorder; prostate disorder; testis disorder; skin disorder; stomach disorder; pancreas disorder; spleen disorder; thymus disorder; thyroid disorder; antiparkinsonian; antimanic; cytostatic; antiinflammatory; vasotrophic; antitumoral; antiarrhythmic; CNS; central nervous system; respiratory; antiatheroeic; antidiabetic; viricide; hepatotropic; antibacterial; antianemic; antiseborrheic; dermatological; antulcer; antihypertoid; antiallergic; anorectic; immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human; gene; ss.

XX	Homo sapiens.
OS	
XX	
PN	WO2004040000-A2.
XX	
PD	13-MAY-2004.
XX	
XX	09-SEP-2003; 2003WO-US028226.
PF	
XX	
XX	09-SEP-2002; 2002US-0409303P.
PR	
PR	09-APR-2003; 2003US-0461329P.
XX	
XX	(PRIM-) PRIMAL INC.
PA	
XX	
PI	Galtanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI	Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX	
DR	WPI; 2004-390329/36.
DR	P-PSDB; ADO29394.
XX	
XX	Novel mammalian G protein coupled receptors, useful for identifying
PT	compounds that modulates diagnosing and treating disease condition
PT	associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT	pectoris, Parkinson's disease.
PT	

Claim 151; SEQ ID NO 1018; 542pp; English.

The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention, methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); musclic disorders; blood disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR-encoding nucleic acid of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at ftn.wipo.int/pub/published pct sequences.

[illegible]

481	Qy	TTCTGCTTCAGAGGACACCGGCACAATTTCAACTCCATCGCGTTCCCGCTGCTGGGATTTC	540
481	Db	TTCTGCTTCAGAGGACACCGGCACAATTTCAACTCCATCGCGTTCCCGCTGCTGGGATTTC	540
541	Qy	TACTCCGCCCTGCGCGTGGTGTCTTCTGCTCCCTGGAAGGTGGTGACTGCGCCCTGGCCCCCAG	600
541	Db	TACTCCGCCCTGCGCGTGGTGTCTTCTGCTCCCTGGAAGGTGGTGACTGCGCCCTGGCCCCCAG	600
601	Qy	AGGCCACCCACCGAGCGTGGGGCAGGCAGAGGCCACCCGCAAGGCTAAACGCATGGTCTGG	660
601	Db	AGGCCACCCACCGAGCGTGGGGCAGGCAGAGGCCACCCGCAAGGCTGGCCGATGGTCTGG	660
661	Qy	GCCAACTCCTGGTGTTCGTGGTGTCTTCTGCTGCCCTGCGCGTGGGGCTGACAGTGGCC	720
661	Db	GCCAACTCCTGGTGTTCGTGGTGTCTTCTGCTGCCCTGCGCGTGGGGCTGACAGTGGCC	720
721	Qy	CTCGCAGTGGGGCTGGAAACGCCCTGTGCCCTCTCTGGAGAGCATCCGCTCGCGGCCCTGTACATA	780
721	Db	CTCGCAGTGGGGCTGGAAACGCCCTGTGCCCTCTCTGGAGAGCATCCGCTCGCGGCCCTGTACATA	780
781	Qy	ACCAGCAAGCTCTCAGATGCCAACTGTGTCCTTGAGCGCCATCTGCTACTACTACATGGCC	840
781	Db	ACCAGCAAGCTCTCAGATGCCAACTGTGTCCTTGAGCGCCATCTGCTACTACTACATGGCC	840
841	Qy	AAGGAGTTCACGAGGCGCTGCACCTGCGCGTGGCTCCCGTGTCTAAGGGCCCAACAAAGC	900
841	Db	AAGGAGTTCACGAGGCGCTGCACCTGCGCGTGGCTCCCGTGTCTAAGGGCCCAACAAAGC	900
901	Qy	CAGGACTCTCTGTGGGTGACCCCTGCCTAA	930
901	Db	CAGGACTCTCTGTGGGTGACCCCTGCCTAA	930

RESULT 6	
ADV73165	
ID	ADV73165 standard; DNA; 930 BP.
XX	
AC	ADV73165;
XX	
DT	10-MAR-2005 (first entry)
XX	
DE	Human colon tumor cell upregulated gene SEQ ID NO 6.
XX	
KW	ds; gene; cancer; neoplasm; cytostatic.
XX	
OS	Homo sapiens.
XX	
PN	WO2004110345-A2.
XX	
PD	23-DEC-2004.
XX	
XX	28-OCT-2003; 2003WO-US034019.
PP	
XX	
PR	29-OCT-2002; 2002US-0422176P.
XX	
PA	(PHAA) PHARMACIA CORP.
XX	
PI	Bourner MJ, Bu JJ, Head RD, Hippenmeyer PJ, Klein BK;
PI	Mazzarella RA, Staten NR;
XX	
DR	WPI; 2005-039958/04.
XX	P-PSDB; ADV73203.
XX	
PT	New antibody that immunospecifically binds to p-cadherin, useful in
PT	preparing a composition for treating or preventing a cancer-associated
PT	disorder.
XX	
PS	Disclosure; SEQ ID NO 6; 257pp; English.
XX	
CC	The invention relates to an antibody immunospecifically binds to p-
CC	cadherin or its fragment. The antibody is useful in preparing a
CC	composition for treating or preventing a cancer-associated disorder. The
CC	present sequence represents a gene upregulated in human colon cancer
CC	

KW non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10;
KW diagnosis; therapy; ss.
OS Homo sapiens.

Key Location/Qualifiers
CDS 576..1505
/*tag=a
/transl_except= (pos:1095..1097, aa:Arg)
/transl_except= (pos:1455..1457, aa:Arg)

WO200023603-A2.

27-APR-2000.

21-OCT-1999; 99WO-US024890.

21-OCT-1998; 98US-0105052P.

13-MAY-1999; 99US-0134175P.

(ARCH-) ARCH DEV CORP.
(TEXA) UNIV OF TEXAS SYSTEM.

Polonsky KS, Horikawa Y, Oda N, Sreenan S, Zhou Y, Otani K;

Hanis CL, Bell GI, Cox NU;

WPI; 2000-339702/29.

P-PSDB; AAY79576, AAY79574, AAY79576.

Method for screening for type 2 diabetes mellitus comprises detecting a polymorphism in a calpain encoding nucleic acid segment or a protease-encoding nucleic acid segment.

Claim 74; Page 238; 257pp; English.

The present sequence corresponds to a transcript of the human gene encoding G protein coupled receptor GPR35 (see AAY79576). The sequence of GPR35 is similar to that of a putative purinoceptor P2Y9 (34.1% identity) suggesting that ATP or other nucleotide is its ligand. GPR35 mRNA was detected in all adult and foetal tissues examined with relatively higher levels in adult lung, small intestine, colon and stomach. In these tissues there are 2 major transcripts of 2.4 and 4.4 kb, whereas in skeletal muscle there is a single transcript of 9.4 kb. The composite cDNA is 1,875 bp (exclusive of polyA tract) and may lack about 400 bp of the 5' untranslated region. The GPR35 gene was identified in a 49,136 bp region (see AAA27475) located within the NIDDM1 region of human chromosome 2. This region also includes the CAPN10 gene, which encodes a novel calpain-like cysteine protease, designated calpain 10. Mutations in the CAPN10 gene are responsible for a propensity to type 2 diabetes. Claimed methods for screening for a propensity for type 2 diabetes mellitus are based on detection of a polymorphism in a calpain encoding nucleic acid. Methods are also claimed for identifying modulators of calpain activity, and using these modulators to treat diabetes, in particular through the regulation of an insulin secretory response or insulin mediated glucose transport

Sequence 1875 BP; 290 A; 593 C; 614 G; 378 T; 0 U; 0 Other;

Query Match 99.0%; Score 920.4; DB 3; Length 1875;
Best Local Similarity 99.4%; Pred. No. 1.9e-174;
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
1 ATGAATGGCACCTTACAAACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCGATCAAG 60
576 ATGAATGGCACCTTACAAACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCGATCAAG 635
61 CTGGGGCTTACGCCCTACTCTGGCGTCTGCTGGCTAGGCTGTGCTCAACACCTG 120
636 CTGGGGCTTACGCCCTACTCTGGCGTCTGCTGGCTAGGCTGTGCTCAACACCTG 695
121 GCGCTCTGGGTGTTCTGCTGCCGATGCAGACGAGACCGCGATCTACATGACC 180
696 GCGCTCTGGGTGTTCTGCTGCCGATGCAGACGAGACCGCGATCTACATGACC 755

QY 181 AACCTGGCGTGGCCGACCTCTCTGCTGCTGTGACCTTGGCCCTTGTGCTGCTACCTG 240
DB 756 AACCTGGCGTGGCCGACCTCTCTGCTGCTGTGACCTTGGCCCTTGTGCTGCTACCTG 815
QY 241 CGAGACACCTTACAGACGCGCTGTGCGACCTTCCCGAGGCGATCTACCTGACCAAGG 300
DB 816 CGAGACACCTTACAGACGCGCTGTGCGACCTTCCCGAGGCGATCTACCTGACCAAGG 875
QY 301 TACATGAGCATCAGCCCTGGTCAAGCCATCGCGTGAACCGCTATGTGGCGCTGCGGCAC 360
DB 876 TACATGAGCATCAGCCCTGGTCAAGCCATCGCGTGAACCGCTATGTGGCGCTGCGGCAC 935
QY 361 CCGCTGCGTGGCCGCGGCTGCGGTCCCGAGGCGTGGCGGCTGTGCGCGTCTC 420
DB 936 CCGCTGCGTGGCCGCGGCTGCGGTCCCGAGGCGTGGCGGCTGTGCGCGTCTC 995
QY 421 TGGGTGCTGTGTCATCGGCTCTGCTGGCTGCTGCTGGGATTCAGGAGGGCGGC 480
DB 996 TGGGTGCTGTGTCATCGGCTCTGCTGGCTGCTGCTGGGATTCAGGAGGGCGGC 1055
QY 481 TTCTGCTTCAGGAGCACCCGCGACAAATTTCAACTCCATGCGGTTCCCGCTGCTGGGATTC 540
DB 1056 TTCTGCTTCAGGAGCACCCGCGACAAATTTCAACTCCATGCGGTTCCCGCTGCTGGGATTC 1115
QY 541 TACCTGCGCTGGCCGCTGTGCTTCTGCTCCCTGAAGGTGGTGAATGCGCTGGCCGACG 600
DB 1116 TACCTGCGCTGGCCGCTGTGCTTCTGCTCCCTGAAGGTGGTGAATGCGCTGGCCGACG 1175
QY 601 AGGCACCCACCGAGTGGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB 1176 AGGCACCCACCGAGTGGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1235
QY 661 GCCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 1236 GCCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1295
QY 721 CTGCGAGTGGGCTGGAGCGCTGTGCGCTCTCTGGAGAGCATCCGCTGCGCGCTGTACATA 780
DB 1296 CTGCGAGTGGGCTGGAGCGCTGTGCGCTCTCTGGAGAGCATCCGCTGCGCGCTGTACATA 1355
QY 781 ACCAGCAAGCTCTCAGATGCGCAACTGTGCTGCTGCGCGCATCTGCTACTACTACATGGCC 840
DB 1356 ACCAGCAAGCTCTCAGATGCGCAACTGTGCTGCTGCGCGCATCTGCTACTACTACATGGCC 1415
QY 841 AAGGAGTTCAGGAGGCGCTGCGACTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 1416 AAGGAGTTCAGGAGGCGCTGCGACTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1475
QY 901 CAGGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 930
DB 1476 CAGGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1505

RESULT 10

ADA84068

ID ADA84068 standard; DNA; 1875 BP.

XX AC

XX AC ADA84068;

XX DT 20-NOV-2003 (first entry)

XX XX

XX DE Human GPR35 gene.

XX XX

KW human; marker; expressed sequence tag; EST; arabidopsis; tumour;

KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;

KW vaccine; ds; gene.

XX OS Homo sapiens.

XX XX

XX PN WO2002103028-A2.

XX XX

XX PD 27-DEC-2002.

```
XX 30-MAY-2002; 2002WO-18004189.
PP
PR 30-MAY-2001; 2001US-02933999P.
PR 22-OCT-2001; 2001US-0330457P.
PR 19-FEB-2002; 2002US-0357144P.
XX
PA (BIOM-) BIOMEDICAL CENT.
XX
PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;
XX WPI; 2003-175241/17.
DR P-PSDB; ADA84069.
XX
PT Determining if a nucleic acid is a marker for a phenotype/cell type of
PT interest, by global comparison of expressed sequence tags known to be
PT expressed in the phenotype/cell type with all ESTs expressed in normal
PT tissue.
XX
PS Claim 23; Page 446-448; 516pp; English.
XX
CC The invention relates to a novel method for determining if a nucleic acid
CC is a marker for a predetermined phenotype/cell type of interest from a
CC biological species. The method comprises performing a global comparison
CC of a group of expressed sequence tags (ESTs) known to be expressed in the
CC phenotype/cell type of interest with all ESTs expressed in normal tissue
CC in order to identify ESTs that are preferentially expressed in the
CC phenotype/cell of interest. A method of the invention is useful for
CC determining whether a nucleic acid is a marker for a predetermined
CC phenotype or cell type of interest from a biological species, preferably
CC Arabidopsis or human. The cell type of interest is an abnormal cell such
CC as a tumour cell, and the predetermined phenotype is a stress-induced
CC phenotype such as hyperosmotic stress or high salt conditions. A method
CC of the invention is also useful for determining the progression of colon
CC cancer in a human, for detecting a tumour cell, and for regulating or
CC preventing the growth of a tumour cell. An antibody of the invention is
CC useful for detecting the absence or presence of peptides encoded by
CC tumour-associated markers. A polypeptide of the invention is useful as an
CC immunogen for vaccinating an animal. The present sequence encodes a
CC tumour-associated antigen of the invention.
XX
SQ Sequence 1875 BP; 290 A; 593 C; 614 G; 378 T; 0 U; 0 Other;

Query Match 99.0%; Score 920.4; DB 8; Length 1875;
Best Local Similarity 99.4%; Pred. No. 1.9e-174;
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGAATGGGACCTTACACACCTGTGGCTCCAGCGACCTCACCTGGCCCGGCGATCAAG 60
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QY 61 CTGGGCTTCTACCCCTACTTGGGCGTCTGTGCTAGGCTGTGCTCAACAGCCCTG 120
DB |||||||
DB 636 CTGGGCTTCTACCCCTACTTGGGCGTCTGTGCTAGGCTGTGCTCAACAGCCCTG 695
QY 121 GCGCTCTGGGTGTCTGTGCTCCGATGCGAGCAGTGGACCGGACCCGCGATCTACATGACC 180
DB |||||||
DB 696 GCGCTCTGGGTGTCTGTGCTCCGATGCGAGCAGTGGACCGGACCCGCGATCTACATGACC 755
QY 181 AACCTGGCGGTGGCGGACCTCTGCTGTGTGACCTTGGCTTGGCTGTGACCTCCCTG 240
DB |||||||
DB 756 AACCTGGCGGTGGCGGACCTCTGCTGTGTGACCTTGGCTTGGCTGTGACCTCCCTG 815
QY 241 CGAGACACCTTCAGACACCGCGCTGTGCCAGCTCTCCGAGGCGATCTACCTGACCAACAGG 300
DB |||||||
DB 816 CGAGACACCTTCAGACACCGCGCTGTGCCAGCTCTCCGAGGCGATCTACCTGACCAACAGG 875
QY 301 TACATGAGCATCAGCTGTGTCAAGGCGATCGCGCTGTGAACCGCTATGTGCCGTGGCGCAC 360
DB |||||||
DB 876 TACATGAGCATCAGCTGTGTCAAGGCGATCGCGCTGTGAACCGCTATGTGCCGTGGCGCAC 935
QY 361 CGGCTGGGTGGCGGCTGGGCTCCCGGACGAGCTGGGCTGGGCTGGGCTGGGCTGGGCT 420
DB |||||||
```

PT compositions for diagnosis and monitoring.
 XX Claim 1; SEQ ID NO 1; 124pp; German.
 XX The invention relates to pharmaceutical compositions that comprise an
 CC agent that inhibits the expression or activity of a tumour-associated
 CC antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical
 CC compositions and related compositions, are used for treatment of diseases
 CC associated with (abnormal) expression of TAG, specifically cancer e.g. of
 CC lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney
 CC or cervix, also melanoma. Compositions containing TAG, or related nucleic
 CC acid, antibodies or host cells, are also useful for diagnosis and
 CC monitoring of tumours. The present sequence represents the human GPR35
 CC DNA.

XX SQ Sequence 1875 BP; 290 A; 593 C; 614 G; 378 T; 0 U; 0 Other;
 Query Match 99.0%; Score 920.4; DB 12; Length 1875;
 Best Local Similarity 99.4%; Pred. No. 1.9e-174;
 Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGAATGGCACTTACAAACCTGTGGCTCCAGCGACCTCAGCTGGCCCCCAGGATCAAG 60
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 Qy 61 CTGGGCTTCTAGCGCTACTTGGGCGTCTGCTGGTGTAGGCTGCTGCTCAACAGCCTG 120
 Db 636 CTGGGCTTCTAGCGCTACTTGGGCGTCTGCTGGTGTAGGCTGCTGCTCAACAGCCTG 695
 Qy 121 CGGCTCTGGGTGTTCTGCTGCGCATGAGCAGTGGAGCGAGCCGCGATCTACATGACC 180
 Db 696 CGGCTCTGGGTGTTCTGCTGCGCATGAGCAGTGGAGCGAGCCGCGATCTACATGACC 755
 Qy 181 AACCTGGCGGTGGCGACCTTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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 Qy 421 TGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 Db 996 TGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1055
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 Qy 541 TACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 Db 1116 TACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1175
 Qy 601 AGGCCACCCAGCAGTGGGGCAGGAGGCGACCCGCAAGGCTTAAGCGATGCTGCTGG 660
 Db 1176 AGGCCACCCAGCAGTGGGGCAGGAGGCGACCCGCAAGGCTGCGCGCTGCTGCTGG 1235
 Qy 661 GCCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 Db 1236 GCCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1295
 Qy 721 CTGCGAGTGGGCTGGAACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 Db 1296 CTGCGAGTGGGCTGGAACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1355

Qy 781 ACCAGCAAGCTCTCAGATGCCAACTGTGCTGCGACGCCATCTGCTACTACTACATGGCC 840
 Db 1356 ACCAGCAAGCTCTCAGATGCCAACTGTGCTGCGACGCCATCTGCTACTACTACATGGCC 1415
 Qy 841 AAGGAGTTCAGAGGCGTCTGCACTGCGCGTGGCTCCCGTGTAAAGGCCCAAAAGC 900
 Db 1416 AAGGAGTTCAGAGGCGTCTGCACTGCGCGTGGCTCCCGTGTAAAGGCCCAAAAGC 1475
 Qy 901 CAGGACTCTCTGTGCTGCGTGACCTCGCCCTAA 930
 Db 1476 CAGGACTCTCTGTGCTGCGTGACCTCGCCCTAA 1505

RESULT 12

AAA27475

ID AAA27475 standard; DNA; 49136 BP.

XX AC AAA27475;

XX DT 15-AUG-2000 (first entry)

XX DE NIDDM1 region including CAPN10 and GPR35 genes.

XX KW NIDDM1; non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10;
 KW GPR35 gene; G protein coupled receptor; human; polymorphism; UCSNP-43;
 KW chromosome 2; diapain-1; diagnosis; therapy; ds.

XX OS Homo sapiens.

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FT exon	5283..5479	
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WO200023603-A2.
27-APR-2000.
21-OCT-1999; 99WO-US024890.
21-OCT-1998; 98US-0105052P.
13-MAY-1999; 99US-0134175P.
(ARCH-) ARCH DEV CORP.
(TEXA ) UNIV OF TEXAS SYSTEM.
Polonsky KS, Horikawa Y, Oda N, Sreenan S, Zhou Y, Otani K;
Hanis CL, Bell GI, Cox NU;
WPI; 2000-339702/29.
P-PSDB; AAV79567, AAV79568, AAV79569, AAV79570, AAV79571, AAV79572,
AAV79573, AAV79574, AAV79576.
Method for screening for type 2 diabetes mellitus comprises detecting a
polymorphism in a calpain encoding nucleic acid segment or a protease-
encoding nucleic acid segment.
Claim 65; Page 203-217; 257pp; English.
The present sequence is that of a 49,136 bp region located within the
NIDDM1 region of human chromosome 2. It includes the CAPN10 gene that
encodes a novel calpain-like cysteine protease, designated calpain 10,
and a gene encoding a G protein coupled receptor, GPR35. Alternative
splicing of calpain 10 mRNA generates a family of proteins. Isoforms 10a-
h (see AAV79567-74) are respectively encoded by exons 1-7,9-13, 1-
7,9,10*,11-13, 1-7,11-13, 1-7,9,11-13, 1-10*,11-13, 1-3*,4-7,9-13,
1,2,14,15 and 1,11-13. Calpain 10 mRNA is ubiquitously expressed; the
major 2.7 kb transcript was detected in every human adult and foetal
tissue examined. Mutations in the CAPN10 gene are responsible for
susceptibility to type 2 diabetes. The nucleotide variant showing all the
evidence for linkage to type 2 diabetes, UCSNP-43, is located at
nucleotide 6225 in intron 3 of the gene. There is alternative splicing of
intron 3, but the molecular mechanism by which the polymorphism at UCSNP-
43 affects susceptibility to type 2 diabetes is unclear. Claimed methods
for screening for a propensity for type 2 diabetes mellitus are based on
detection of a polymorphism in a calpain encoding nucleic acid,
especially UCSNP-10 of the CAPN10 gene. Methods are also claimed for
identifying modulators of calpain activity using calpain 10 polypeptides
and nucleic acids, and using these modulators to treat diabetes, in
particular through the regulation of an insulin secretory response or
insulin mediated glucose transport
XX Sequence 49136 BP; 10300 A; 13118 C; 14165 G; 11553 T; 0 U; 0 Other;
Query Match      99.0%; Score 920.4; DB 3; Length 49136;
Best Local Similarity 99.4%; Pred. No. 2.7e-174;
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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DB      43645 ATGAATGCACCTACACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCGCATCAAG 43704
QY      61 CTGGCTTCTACGGCTACTTGGGGCTCTGTGGTGTCTAGGCTGTGCTCAACAGCCTG 120
DB      43705 CTGGCTTCTACGGCTACTTGGGGCTCTGTGGTGTCTAGGCTGTGCTCAACAGCCTG 43764
QY      121 GCGCTCTGGGTGTTCTGCTGCCGATGACGAGTGGAGACCCGCACTACATGACC 180
DB      43765 GCGCTCTGGGTGTTCTGCTGCCGATGACGAGTGGAGACCCGCACTACATGACC 43824
QY      181 AACCTGGGGTGGCGGACCTCTGCTGTGCACCTTGGCTTGGCTGTGCTGCTCCCTG 240
|||||
```


QY	841	AAGGAGTTCCAGGAGGGCTCTGCACTGGCCGTGGCTCCCGTCTAAGGCCCAAAAAGC	900
DB	3352	AAGGAGTTCCAGGAGGGCTCTGCACTGGCCGTGGCTCCCGTCTAAGGCCCAAAAAGC	3411
QY	901	CAGGACTCTCTGTGGTGACCCCTGCCTAA	930
DB	3412	CAGGACTCTCTGTGGTGACCCCTGCCTAA	3441
RESULT 15			
AAZ35390			
ID	AAZ35390 standard; cDNA; 1043 BP.		
XX			
AC	AAZ35390;		
XX			
DT	11-APR-2000 (first entry)		
XX			
DE	Human G-protein coupled receptor GPR35A cDNA.		
XX			
KW	GPR35A; human; G-protein coupled receptor; purinergic;		
KW	7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic;		
KW	cytostatic; antidiabetic; anorectic; antiaethmatic; antiparkinsonian;		
KW	hypotensive; hypertensive; osteopathic; antianginal; cardiac;		
KW	cerebroprotective; antitumor; antiallergic; antimigraine; antiemetic;		
KW	tranquillizer; antidepressant; neuroleptic; nootropic; anticonvulsant;		
KW	gene therapy; diagnosis; vaccine; ss.		
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PR	11-JUN-1999;	98US-00096031.	
XX			
PA	(SMIK) SMITHKLINE BEECHAM CORP.		
XX			
PI	Elsehourbagy NA;		
XX			
DR	WPI; 2000-116525/10.		
DR	P-PSDB; AAZ35390.		
XX			
PT	New human GPR35A polypeptides and polynucleotides used to identify agonists, antagonists and inhibitors for use in therapy.		
XX			
PS	Claim 2; Page 32; 38pp; English.		
XX			
CC	The present sequence represents cDNA coding for human GPR35A (see		
CC	AAV58645), a novel member of the purinergic family of polypeptides and a		
CC	G-protein coupled receptor. The invention provides GPR35A polynucleotides		
CC	having at least 70% identity with the present sequence. GPR35A		
CC	polypeptides, recombinant materials, and methods for their production.		
CC	GPR35A polypeptides can be used for identifying agonists and		
CC	antagonists/inhibitors, and for detecting diseases associated with		
CC	inappropriate GPR35A activity or levels. GPR35A polypeptides and		
CC	polynucleotides, agonists, antagonists and antibodies are used to treat:		
CC	infections such as bacterial, fungal, protozoan and viral infections, such		
CC	particularly HIV-1 and HIV-2; pain; cancer; diabetes; obesity; anorexia;		
CC	bulimia; asthma; Parkinson's disease; acute heart failure; hypotension;		
CC	hypertension; urinary retention; osteoporosis; angina pectoris;		
CC	myocardial infarction; stroke; ulcers; allergy; benign prostatic		
CC	hypertrophy; migraine; vomiting; psychotic and neurological disorders		
CC	including anxiety, schizophrenia, manic depression, depression, delirium,		
CC	dementia and severe mental retardation; and dyskinesias such as		
CC	Huntington's or Gilles de la Tourette's syndrome. The polynucleotide is		
CC	also useful as a source of primers and probes, and also for detecting the		

[illegible]

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Job time : 691 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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(without alignments)

9560.973 Million cell updates/sec

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Perfect score: 930

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

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2: gb_est2.*
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10: gb_gss2.*
11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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C 2	736.4	79.2	876	7 CN834209	CN834209 AGENCOURT
C 3	674.2	72.5	906	7 CN835542	CN835542 AGENCOURT
C 4	609.8	65.6	960	7 CN843697	CN843697 AGENCOURT
C 5	601.2	64.6	750	7 CO921172	CO921172 AGENCOURT
C 6	591.2	63.6	642	10 AY401608	AY401608 Pan trogl
C 7	581.8	62.6	778	7 CO923163	CO923163 AGENCOURT
C 8	571	61.4	759	7 CO957219	CO957219 AGENCOURT
C 9	549.2	59.1	924	10 AY401609	AY401609 Mus muscu
10	549.2	59.1	2649	4 AK036503	AK036503 Mus muscu
11	544.4	58.5	3158	4 AK034870	AK034870 Mus muscu
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C 21	392.6	42.2	614	9 BZ221309	BZ221309 CH230-312
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23	374.4	40.3	701	5	BY748928	BY748928
C 24	338.4	36.4	372	2	BF766676	CM3-CS004
C 25	335.4	36.1	736	1	AI861901	AI861901 tcl1f02.x
C 26	317.6	34.2	444	1	AW854188	AW854188 RC3-CT025
C 27	317	34.1	429	1	AW854178	AW854178 RC3-CT025
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29	313.4	33.7	648	7	CO957232	AGENCOURT
C 30	308	33.1	457	1	AW854180	AW854180 RC3-CT025
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C 32	307	33.0	554	2	BE696076	BE696076 RC3-CT025
C 33	305.6	32.9	351	1	AW854187	AW854187 RC3-CT025
C 34	300.8	32.3	448	1	AW854198	AW854198 RC3-CT025
C 35	297.4	32.0	437	1	AW854203	RC3-CT025
C 36	296	31.8	411	1	AW854204	AW854204 RC3-CT025
C 37	296	31.8	571	2	BE696051	BE696051 RC3-CT025
C 38	293.4	31.5	459	1	AW854197	AW854197 RC3-CT025
C 39	293.4	31.5	701	6	CB321988	CB321988 UI-CF-PN0
C 40	293	31.5	585	1	AW854051	RC3-CT025
C 41	290.6	31.2	368	2	BF764582	BF764582 CM3-CS004
C 42	286.6	30.8	647	7	CN790753	CN790753 4125379 B
C 43	285.6	30.7	325	2	BF764700	CM3-CS004
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ALIGNMENTS

RESULT 1	AY401607	Homo sapiens GPR35 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.	930 bp	DNA	linear	GSS 15-DEC-2003
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LOCUS						
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VERSION						
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ORIGIN						
Query Match						
Best Local Similarity						
Matches						
Conservative						
Mismatches						
Indels						
Gaps						

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Db 121 GCGCTCTGGGTGTTCTGCTGCCCATGCAAGCATGGAAGGACCCGCACTTCAATGACC 180
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Db 301 TACATGAGCATCAGCTGCTGTCAGCGCATGCGCGTGAACCGCTATGTGCGCGTGGCGCAC 360
QY 361 CCGCTCGGTGCGCGCGGCTGCGGTGCGCGGACGCTGCGCGCTGTGCGCGGTCTCTC 420
Db 361 CCGCTCGGTGCGCGCGGCTGCGGTGCGCGGACGCTGCGCGCTGTGCGCGGTCTCTC 420
QY 421 TGGGTGCTGCTCATCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 TGGGTGCTGCTCATCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 TTCTGCTTTCAGGACGACCGCGCAAAATTTCAATCCATGCGGTTCCTGCTGCTGGATTTC 540
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QY 601 AGGCCACCCACCGACCTGCGGACGAGGACCGACCGGACGCTAAACGCACTGCTG 660
Db 601 AGGCCACCCACCGACCTGCGGACGAGGACCGACCGGACGCTAAACGCACTGCTG 660
QY 661 GCCAACCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 GCCAACCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 CTGCGAGTGGGCTGGAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 CTGCGAGTGGGCTGGAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 ACCAGCAAGCTCTCAGATGCCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 781 ACCAGCAAGCTCTCAGATGCCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 AAGGAGTTCAGGAGCGCTGCACTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 AAGGAGTTCAGGAGCGCTGCACTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 901 CAGGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 930
Db 901 CAGGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 930
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RESULT 2

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CN834209/c
LOCUS
DEFINITION CN834209 15864200 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:7001934 3', mRNA sequence.
ACCESSION CN834209
VERSION CN834209.1 GI:47938609
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KEYWORDS

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 (bases 1 to 876)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: GPCR Consortium

cDNA Library Preparation: GPCR Consortium

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Cloned by: Agencourt Bioscience Corporation

Cloned through the MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: IRB13 row: a column: 04

High quality sequence start: 4

High quality sequence stop: 650.

FEATURES

Location/Qualifiers

1..876

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:7001934"

/tissue_type="mixed"

/lab_host="DH10B"

/clone_lib="NIH MGC 145"

/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:

varies by clone; ORFs were PCR-amplified and cloned into

pCDNA3.1 by the GPCR Consortium. Cloning sites vary by

clone and include the following: 5'-EcoRV-XbaI/XhoI-3',

5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).

For information about which gene each clones represents,

please visit our anonymous ftp site at

ftp://image.llnl.gov/image/rearrayed_plates/IRB1.preSV.dat

a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 79.2%; Score 736.4; DB 7; Length 876;
Best Local Similarity 97.7%; Pred. No. 2.1e-150;
Matches 765; Conservative 0; Mismatches 16; Indels 2; Gaps 2;

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QY 141 CCGCATGCGAGTGGACGAGAC-CCGCACTCTACATGACCAACC-TGGCGGTGGCCGAC 198
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QY 199 CTCTGCTGCTGTCACCTTGGCCCTTGGTGTGCACTCCCTCGAGACACCTCAGACAG 258
Db 727 TTCTGCTGCTGTCACATTTGCTTGTGCTGCACTCCCTCGAGACACTTACAGACAG 668
QY 259 CCGCTGTGTCAGCTCTTCCAGGGCATCTACCTGACCAACAGGTACTATGAGCATCAGCTG 318
Db 667 CCGCTGTGTCAGCTCTTCCAGGGCATCTACCTGACCAACAGGTACTATGAGCATCAGCTG 608
QY 319 GTACAGGCGCATCGCGTGGACCCGCTATGTGGCGGTGGGCAACCGCTGGCGCCCGGG 378
Db 607 GTACAGGCGCATCGCGTGGACCCGCTATGTGGCGGTGGGCAACCGCTGGCGCCCGGG 548
QY 379 CTGGCGTCCCCCAGGAGGCTGGCGCGGTGTCCTCTGCTGCTGCTGCTGCTGCTGCTG 438
Db 547 CTGGCGTCCCCCAGGAGGCTGGCGCGGTGTCCTCTGCTGCTGCTGCTGCTGCTGCTG 488
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Qy 499 CGGCACAAATTTCAACTCATCGGTTCCCGCTGCTGGGATTTCTACTGCGCCCTGGCCGCTG 558
Dy 427 CGGCACAAATTTCAACTCATCGGTTCCCGCTGCTGGGATTTCTACTGCGCCCTGGCCGCTG 368
Qy 559 GTGGTCTTCTGCTCCCTGAAGTGTGATCCCTGCGCCGAGGCGCACCCACCGAGTG 618
Dy 367 GTGGTCTTCTGCTCCCTGAAGTGTGATCCCTGCGCCGAGGCGCACCCACCGAGTG 308
Qy 619 GGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 678
Dy 307 GGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 248
Qy 679 GTGGTCTTCTGCTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 738
Dy 247 GTGGTCTTCTGCTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 188
Qy 739 GCCTGTGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 798
Dy 187 GCCTGTGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 128
Qy 799 GCGAAGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 858
Dy 127 GCGAAGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 68
Qy 859 TCTGACAGGCGGCTGCTCCCGCTGCTAAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 918
Dy 67 TCTGACAGGCGGCTGCTCCCGCTGCTAAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 8
Qy 919 ACC 921
Dy 7 CCC 5
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RESULT 3
LOCUS CN835542/c
DEFINITION AGENCOURT 15864184 NIH MGC 145 Homo sapiens cDNA clone
IMAGE:7001933 3', mRNA sequence.
ACCESSION CN835542
VERSION CN835542.1 GI:47941197
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 906)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB13 row: a column: 03
High quality sequence stop: 634.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7001933"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_lib="NIH_MGC_145"
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ORIGIN
Query Match 72.5%; Score 674.2; DB 7; Length 906;
Best Local Similarity 91.9%; Pred. No. 8.4e-137; Indels 2; Gaps 2;
Matches 734; Conservative 0; Mismatches 63;
Qy 120 GGGCTCTGGGTGTTCTGCTGCGCATGTCAGCAGTGCAGCGACGACGACCGCGCATCTATCATGAC 179
Dy 801 GGTGTTTGGCTGGCCGCTGCAAGCTGTCAGAGCTGGAGCGGAGCGCCGCGCTGTACATGACCC 742
Qy 180 CAACCTGGCGGTGGCCG-ACCTCTGCTGCTGTGTGACCTTGGCCCTT-CGTGCTGCACTCC 237
Dy 741 AACGAGGGGTTGGCCGAACTCTACATGCTGAGCACTTGGCCATTTGCGTGTGATGCGATCC 682
Qy 238 CTGCGAGACACTCAGACACGCGCTGTGCGAGCTCTCCGAGGCGATCTACCTGACCAAC 297
Dy 681 GTGCGAGGACATCAGACACGCGCTGTGCGAGCTCTGCGAGGCGATGTGCATGACCAAC 622
Qy 298 AGGTACATGAGCATCAGCTGTTCAAGCGCCATCCCGCTGAGCCGCTATGTGGCGGTGGCG 357
Dy 621 AGGTACATGAGCATCAGCTGTTCAAGCGCCATCCCGCTGAGCCGCTATGTGGCGGTGGCG 562
Qy 358 CACCGCTGCTGCGCGCGCTGCGGTTCGCCAGGAGGCTGCGGCGGTGTGCGCGGTGTC 417
Dy 561 CACCGCTGCTGCGCGCGCTGCGGTTCGCCAGGAGGCTGCGGCGGTGTGCGCGGTGTC 502
Qy 418 CTCTGGGTGCTGTGTCATGCGCTCCCTGGTGGCTGCTGGCTCTCTGGGAGTTTCAGAGGGC 477
Dy 501 CTCTGGGTGCTGTGTCATGCGCTCCCTGGTGGCTGCTGGCTCTCTGGGAGTTTCAGAGGGC 442
Qy 478 GGGTCTGCTTTCAGGAGCACCGCGCACAAATTTCAACTCTCATGCGGTTTCCCGCTGTGGGA 537
Dy 441 GGGTCTGCTTTCAGGAGCACCGCGCACAAATTTCAACTCTCATGCGGTTTCCCGCTGTGGGA 382
Qy 538 TTCTACCTGCGCCCTGGCGGTGCTGTCTCTGCTCCCTGAAGGTTGTCATGCTGCGCTGGCC 597
Dy 381 TTCTACCTGCGCCCTGGCGGTGCTGTCTCTGCTCCCTGAAGGTTGTCATGCTGCGCTGGCC 322
Qy 598 CAGAGGCCACCCACCGAGCGTGGGCGAGCGAGGCGCACCCGCAAGGCTAAACGCGATGGTC 657
Dy 321 CAGAGGCCACCCACCGAGCGTGGGCGAGCGAGGCGCACCCGCAAGGCTAAACGCGATGGTC 262
Qy 658 TGGGCGCAACCTCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
Dy 261 TGGGCGCAACCTCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 202
Qy 718 CGCCTCGCAGTGGGCTGGAAAGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 777
Dy 201 CGCCTCGCAGTGGGCTGGAAAGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 142
Qy 778 ATAACGAGCAAGCTCTCAGATGCCAACTGTGCTGCTGCGCGCATCTGCTACTACTACATG 837
Dy 141 ATAACGAGCAAGCTCTCAGATGCCAACTGTGCTGCTGCGCGCATCTGCTACTACTACATG 82
Qy 838 GCCAAGGAGTTCCAGGAGCGCTGTCACATGGCGGTGGCTCCCGCTGCTAAAGCCGCCACAAA 897
Dy 81 GCCAAGGAGTTCCAGGAGCGCTGTCACATGGCGGTGGCTCCCGCTGCTAAAGCCGCCACAAA 22
Qy 898 AGCCAGGAGCTCTCTGTGG 916
Dy 21 AGCCAGGAGCTCTCTGTGG 3
RESULT 4
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/notes="Vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRB1.preSV.dat a Note: this is a NIH_MGC Library."

ftp://image.llnl.gov/image/rearranged_plates/IRBI.presv.dat
a Note: this is a NIH_MGC Library."

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ORIGIN
Query Match      64.6%; Score 601.2; DB 7; Length 750;
Best Local Similarity 97.0%; Pred. No. 7.5e-121;
Matches 612; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 300 GTACATGAGCATCAGCTGGTCACGGCCATCGCGTGGACCGCTATATGGCCGTCGCGCA 359
Db 668 GTACATGAGCATCAGCTGGTCACGGCCATCGCGGACCGTTATGTCGCGTGCCTT 609
Qy 360 CCCCTGCTGCTCCCGCGGCTCGCGTCCCCAGACAGGCTGCGCCGCTGCGCGGCTCT 419
Db 608 CCCGTTGCTGCTCCCGCGGCTCGCGTCCCCAGGACAGGCTGCGCGGCTGCGCGGCTCT 549
Qy 420 CTGGGTGCTGCTCATCGGCTCCCTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
Db 548 CTGGGTGCTGCTCATCGGCTCCCTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 489
Qy 480 CTTCTGCTTTCAGGAGCACCGCGCACAAATTCATCTCATGCGGTTCCCGCTGCTGGGATT 539
Db 488 CTTCTGCTTTCAGGAGCACCGCGCACAAATTCATCTCATGCGGTTCCCGCTGCTGGGATT 429
Qy 540 CTACTGCGCCCTGGCGGCTGGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
Db 428 CTACTGCGCCCTGGCGGCTGGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 369
Qy 600 GAGGCGACCCACCGAGCTGGGCGGAGGAGGCGACCCGCAAGGCTAAACGATGCTGTG 659
Db 368 GAGGCGACCCACCGAGCTGGGCGGAGGAGGCGACCCGCAAGGCTGCGCCATGCTGTG 309
Qy 660 GGCCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 719
Db 308 GGCCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 249
Qy 720 CTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779
Db 248 CTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 189
Qy 780 AACGACGAGCTCTCAGATGCGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839
Db 188 AACGACGAGCTCTCAGATGCGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 129
Qy 840 CAAGAGTTCCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
Db 128 CAAGAGTTCCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 69
Qy 900 CCAGGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 930
Db 68 CCAGGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 38
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RESULT 6
AY401608
LOCUS AY401608 642 bp DNA linear GSS 15-DEC-2003
DEFINITION Pan troglodytes GPR35 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION AY401608
VERSION AY401608.1 GI:39757597
KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.

REFERENCE 1 (bases 1 to 642)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 642)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
DIRECT SUBMISSION
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
source Location/Qualifiers
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ORIGIN

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Best Local Similarity 93.3%; Pred. No. 1.1e-118;
Matches 599; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 1 ATGAATGGCACTACAAACACCTGTGGTCTCAGCACCTCACCTGGCCCCCAGGATCAAG 60
Db 1 ATGAATGGCACTACAAATANNNTGTGGCTCCAGTGANNTCANNTGGCCCCCAACATCAAG 60
Qy 61 CTGGGCTTTACGGCTACTTGGGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Db 61 CTCGNNNNNNCGCTACTTGGGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Qy 121 GCGCTCTGGGTGTTCTGCTGCGCATGCGAGTGGAGCGAGACCGCATCTACATGACC 180
Db 121 GCGCTCTGGGTGTTCTGCTGCGCATGCGAGTGGAGCGAGACCGNNNNNNCATGACC 180
Qy 181 AACCTGGCGGTGGCGGACCTCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db 181 AACCTGGCGGTGGCGGACCTCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Qy 241 CGAGACACCTCAGACACGCGCTGTGCGAGCTCTCCGAGGGGATCTACTGACCAACAGG 300
Db 241 CGAGACACCTCAGACACGCGCTGTGCGAGCTCTCCGAGGGGATCTACTGACCAACAGG 300
Qy 301 TACATGAGCATCAGCTGTTCAAGGCTGTTCAAGGCTGTTCAAGGCTGTTCAAGGCTGTT 360
Db 301 TACATGAGCATCAGCTGTTCAAGGCTGTTCAAGGCTGTTCAAGGCTGTTCAAGGCTGTT 360
Qy 361 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 361 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy 421 TGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 TGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy 481 TTCTGCTTTCAGGAGCACCGGCGACAAATTTCAACTCATGCGGTTCCCGCTGTGCGATTTC 540
Db 481 TTCTGCTTTCAGGAGCACCGGCGACAAATTTCAACTCATGCGGTTCCCGCTGTGCGATTTC 540
Qy 541 TACCTGCCCCCTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 TACCTGCCCCCTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Qy 601 AGGCCACCCACCGAGCTGGGGCAGGACAGAGGCCACCCCGCAAG 642
Db 601 AGGCCACCCACCGAGCTGGGGCAGGACAGAGGCCACCCCGCAAG 642
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RESULT 7
C0923163


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Query Match      61.4%; Score 571; DB 7; Length 759;
Best Local Similarity 98.5%; Pred. No. 3e-114;
Matches 607; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

Qy 316 CTGCTCAGCGCCATCGCCGTGAGACCGCTATGTGCGCGTGGGACACCGCGTGGCGCCG 375
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Db 635 CTGCTCAGCGCCATCGCCGTGAGACCGCTATGTGCGCGTGGGACACCGCGTGGCGCCG 576
    |||||

Qy 376 GGGCTGGCGTCCCGCAGGAGCGTGGCGCGTGGCGCGTGGCGTGGCGTGGCGTGGCGTATC 435
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Db 575 GGGCTGGCGTCCCGCAGGAGCGTGGCGCGTGGCGCGTGGCGTGGCGTGGCGTGGCGTATC 516
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Qy 436 GGGCTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGT 495
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Db 515 GGGCTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGT 456
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Qy 496 ACCCGGACAAATTTCAATCCATCGGTTCCCGTGTGGGATTTACCTGCCCTGGCC 555
    |||||
Db 455 ACCCGGACAAATTTCAATCCATCGGTTCCCGTGTGGGATTTACCTGCCCTGGCC 396
    |||||

Qy 556 GTGCTGCTTCTGCTCCCTGAAGGTGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614
    |||||
Db 395 GTGCTGCTTCTGCTCCCTGAAGGTGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 336
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Qy 615 CGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 673
    |||||
Db 335 CGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 276
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Qy 674 TGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 733
    |||||
Db 275 TGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 216
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Qy 734 GGAACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 793
    |||||
Db 215 GGAACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 156
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Qy 794 CAGATGCCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853
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Db 155 CAGATGCCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 96
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Qy 854 AGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 913
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Db 95 AGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 36
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Qy 914 GCGTGACCTCGCCTA 929
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Db 35 GCG-GACCTCGCCTA 21
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RESULT 9
LOCUS AY401609
DEFINITION Mus musculus GPR35 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION AY401609
VERSION AY401609.1 GI:39757598
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 924)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity 77.7%; Pred. No. 1.8e-109;
Matches 704; Conservative 0; Mismatches 193; Indels 9; Gaps 3;

Qy 30 CAGGACCTCAGCTGGCCCCAGGATCAAGCTGGGCTTCTACGCTTCTGCGGCTTCTGCGGCTCT 89
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Db 21 CAGCACCTCAGCTGGGCTGCTTCCGTCACACACTTCTTCATCATCTACTCAGCCTTGGCT 80
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Qy 90 GCTGTGCTAGGCTGCTGCTCAACAGCTGGGCTTCTGGGTGTTCTGTGCTGCTGCTGCTGCTGCT 149
    |||||
Db 81 GCTGTGCTGGGCTGCTGCTCAACAGCTGGGCTTCTGGGTATTTCTGCTATTCGATGCTGCTGCT 140
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Qy 150 GCAGTGACGAGACCGGCTATCTACATGACCAACCTGGCGTGGCGGCTGCTGCTGCTGCTGCTGCT 209
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Db 141 CCAGTGACGAGACCGGCTATCTATATGACCAACCTGGCTGGCGGCTGCTGCTGCTGCTGCTGCT 200
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Qy 210 GTGCACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 266
    |||||
Db 201 CTGCTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 260
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Qy 267 CCAGCTTCCGAGGCTTACCTGACCAACAGCTGATGAGCATGAGCTGAGCTGAGCTGAGCTGAGCTG 326
    |||||
Db 261 CCAGCTTCCAGGCTTACCTGAGCAACAGATATATGAGCATGAGCTGAGCTGAGCTGAGCTGAGCT 320
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Qy 327 CATCGCTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 386
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Db 321 CATGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 380
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Qy 387 CCCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 446
    |||||
Db 381 CCCGAGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 440
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Qy 447 GGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 503
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Db 441 AGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 500
    |||||

Qy 504 CAATTTCAATCCATGCGTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 563
    |||||
Db 501 CAATTTCAATCCATGCGTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
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Qy 564 CTCTGCTCCCTGAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 623
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Db 561 CTCTGCTCTTTTCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620
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Qy 624 GCGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683
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Qy 684 CTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 743
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Db 741 TGCTGCCGAGACACCTTCAGCGTGCCTGTCCATCCACAGGTAAACTCTCAGACACCAA 800

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Qy 864 ACTGGCGTGGCTCCCGTCTTAAGGCCCAAAAGCCAGGACTCTCTGTGGTGGACCT 923

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Qy 924 GGCCTA 929

Db 918 CACCTA 923

RESULT 10

AK036503

LOCUS

DEFINITION

AK036503 2649 bp mRNA linear HTC 03-APR-2004

Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830121M19 product:G protein-coupled receptor 35, full insert sequence.

AK036503

VERSION

KEYWORDS

SOURCE

ORGANISM

AK036503.1 GI:26331445

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalisation and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Iehi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

11076861

4

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2649)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/

URL:http://fantom.gsc.riken.jp/.

Location/Qualifiers

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ORIGIN

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Best Local Similarity 77.7%; Pred. No. 28-109;

Matches 704; Conservative 0; Mismatches 193; Indels 9; Gaps 3;

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QY 90 GCTGTGTCTAGGCTGCTGCTCAACAGCGCTGGCGCTCTGGGTGTTCTGTGCGCGATGCA 149

Db 252 GCTGTGTCTGGCGCTGCTGCTCAACAGCGCTGGCAGCTTGGGTATTCTGCTATCGCATGCA 311

QY 150 GCAGTGGAGGAGACCGGATCTACATGACCACTGGCGGTGGCGGCTCTGCTGCTGCT 209

Db 312 CCAGTGGACAGAGACCGGATCTATATGACCACTGGCGGTGGCGGCTCTGCTGCTGCT 371

QY 210 GTGCACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 266

Db 372 CTGCTCTTGGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 431

QY 267 CCAGCTCTCCAGGGGATCTACTGACCAACAGGTACATGAGCATCAGCTGTGTACCGGC 326

Db 432 CCAGCTCTCAGAGGGATCTACTGCTGGCCAAAGATAGATGAGCATAAGCTGTGTACTGC 491

QY 327 CATCGCGGTGGACCGCTATGTGGCGTGGCGCACCGCTGCTGCGCGGGGTGCGGCTC 386

[illegible]

RESULT 11	AK034870	LOCUS	AK034870	3158 bp	mRNA	linear	HTC 03-APR-2004
DEFINITION			Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430051L15				
			product:G protein-coupled receptor 35, full insert sequence.				
ACCESSION			AK034870				
VERSION			AK034870.1	GI:26330261			
KEYWORDS			HTC; CAP trapper.				
SOURCE			Mus musculus (house mouse)				
ORGANISM			Mus musculus				
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE			1	Carninci, P. and Hayashizaki, Y.			
AUTHORS				High-efficiency full-length cDNA cloning			
TITLE				Meth. Enzymol. 303, 19-44 (1999)			
JOURNAL				10349636			
PUBMED							
REFERENCE			2	Carninci, P., Shibata, Y., Hayatsu, M., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
AUTHORS				Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
TITLE				Genome Res. 10 (10), 1617-1630 (2000)			
JOURNAL				11042159			
PUBMED							
REFERENCE			3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,			
AUTHORS							

TITLE	Sumi, N., Iehii, Y., Nakamura, S., Hazama, M., Sakaguchi, S., Ikegami, T., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, K., Fujiwara, S., Inoue, K., Ogawa, K., Tanaka, T., Matsura, S., Kawai, J., Onoda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
JOURNAL	RIKEN integrated sequence analysis (RISA) system-384-format
PUBMED	sequencing pipeline with 384 multicapillary sequencer
REFERENCE	Genome Res. 10 (11), 1757-1771 (2000)
AUTHORS	11076861
TITLE	4
JOURNAL	The RIKEN Genome Exploration Research Group Phase II Team and the
PUBMED	FANTOM Consortium.
REFERENCE	Functional annotation of a full-length mouse cDNA collection
AUTHORS	Nature 409, 685-690 (2001)
TITLE	5
JOURNAL	The FANTOM Consortium and the RIKEN Genome Exploration Research
PUBMED	Group Phase I & II Team.
REFERENCE	Analysis of the mouse transcriptome based on functional annotation
AUTHORS	of 60,770 full-length cDNAs
TITLE	Nature 420, 563-573 (2002)
JOURNAL	6 (bases 1 to 3158)
PUBMED	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
REFERENCE	Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
AUTHORS	Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
TITLE	Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
JOURNAL	Katoh, H., Kawahara, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
PUBMED	Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
REFERENCE	Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
AUTHORS	Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
TITLE	Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
JOURNAL	Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akai, S.,
PUBMED	Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,
REFERENCE	Muramatsu, M. and Hayashizaki, Y.
AUTHORS	Direct Submission
TITLE	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
JOURNAL	Physical and Chemical Research (RIKEN), Laboratory for Genome
PUBMED	Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
REFERENCE	RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama
AUTHORS	Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
TITLE	URL: http://genome.gsc.riken.jp/ , Tel: 81-45-503-9222,
JOURNAL	Fax: 81-45-503-9216)
PUBMED	cDNA library was prepared and sequenced in Mouse Genome
REFERENCE	Encyclopedia Project of Genome Exploration Research Group in Riken
AUTHORS	Genomic Sciences Center and Genome Science Laboratory in RIKEN.
TITLE	Division of Experimental Animal Research in Riken contributed to
JOURNAL	prepare mouse tissues.
PUBMED	Please visit our web site for further details.
REFERENCE	URL: http://genome.gsc.riken.jp/
AUTHORS	URL: http://fantom.gsc.riken.jp/

FEATURES

CDS

```
neck"
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Matches 701; Conservative	0; Mismatches 196; Indels 9; Gaps 3;	
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QY	684 CTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	743
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Db	934 TGCCTTCTGAGAGCATCGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	993
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Db	994 CTGCTGCTGAGAGCATCGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1053
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Db	1054 GCGAGGAGCTGCTTCC---AAGACACCCACAGAGGCAATATTCAGATCTGAGCTT	1110
QY	924 CCGCTTA 929	
Db	1111 CACCTA 1116	

RESULT 12	AK089198
LOCUS	
DEFINITION	
ACCESSION	AK089198.1 GI:26105132
VERSION	HTC; CAP trapper.
KEYWORDS	Mus musculus (house mouse)
SOURCE	Mus musculus
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349636
AUTHORS	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 11042159
TITLE	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuani, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861
JOURNAL	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
PUBMED	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 4254) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurahara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sobabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
AUTHORS	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
TITLE	864 ACTGGCGCTGGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
JOURNAL	1054 GCGAGGAGCTTCC---AAGACACCCACAGAGGCAATATTCAGATCTGAGCTT

COMMENT

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>

FEATURES

source
1. 4254
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/strain="NOD"
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ORIGIN

Query Match 57.9%; Score 538.2; DB 4; Length 4254;
Best Local Similarity 77.6%; Pred. No. 5.2e-107; Indels 10; Gaps 4;
Matches 704; Conservative 0; Mismatches 193;

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DB	808	CCGAGACAGGCTGACGAGGTGTGTGGCCCTTTGGGTGATGTGTCACTCCCTGGT	867
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QY	564	CTTCTGCTCCCTGAGAGTGTGACATGCTGCTGCCCGCAGAGGCCACCCACCGAGCTGGGCA	623
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QY	624	GGCAGAGCCACCCGCAAGGCTAAACGCATGTGTCTGGGCGCACTCTCTGGTGTCTGGT	683
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QY	684	CTGCTTCTGCGCCCTGCACGTGGGGCTGACAGTGGCGCTCGCAGTGGCTGGAGCGCTG	743
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QY	744	TGCGCTCTGGAGACCATCGTCGCGCCCTGTACATAACCCAGCAAGCTCTCAGATGCCAA	803
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DB	1228	GCTGCTGCTGGATGCACTGTACTACTATACATGGCCAGAGAGTTTCAGAGGCGCTCA	1287
QY	863	CAGTGGCGGTGCTCCCGCTGCTAAGGCCACAAAAGCCAGGACTCTCTGTGCGTACCC	922
DB	1288	AGCAGCCAGCTCTTCC---AACACACACCCCAAGAGCAAGATTCCAGATCCTGAGCC	1344
QY	923	TCGCGCTA 929	
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RESULT 13

CN835586
LOCUS
DEFINITION
AGENCOURT_15669742 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:7001933 5', mRNA sequence.

ACCESSION
CN835586

VERSION
CN835586.1 GI:47941241

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 783)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs-r@mail.nih.gov

Tissue Procurement: GPCR Consortium

cDNA Library Preparation: GPCR Consortium

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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High quality sequence stop: 482.

Location/Qualifiers

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/clone_lib="NIH_MGC_145"

/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:

varies by clone; ORFs were PCR-amplified and cloned into

pCDNA3.1 by the GPCR Consortium. Cloning sites vary by

clone and include the following: 5'-EcoRV-XbaI/XhoI-3',

5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional).

For information about which gene each clones represents,

please visit our anonymous ftp site at

ftp://image.llnl.gov/image/rearrayed_plates/IRBI.presv.dat

a Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match

57.1%; Score 531.2; DB 7; Length 783;

Best Local Similarity 94.2%; Pred. No. 1.5e-105;
Matches 585; Conservative 0; Mismatches 29; Indels 7; Gaps 3;
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QY 61 CTGGGCTTCTACGCTTACTTGGGCTTCCTGGTGTGCTAGGCTGTCTCAACAGCCTG 120
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IMAGE:7211810 3', mRNA sequence.
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EST.
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 717)
NIH-MGC Institute://img.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB15 row: b column: 12
High quality sequence stop: 478.
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/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1.preSV.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 55.5%; Score 516.6; DB 7; Length 717;
Best Local Similarity 96.4%; Pred. No. 2.3e-102;
Matches 539; Conservative 0; Mismatches 19; Indels 1; Gaps 1;
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QY 552 GCGCGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 611
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CN832122/c

[illegible]

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	111.6	12.0	1098	3	US-09-170-496D-225
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6	111.2	12.0	1365	3	US-09-016-434-1429
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8	110	11.8	1098	3	US-09-170-496D-117
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10	110	11.8	1597	2	US-08-724-974A-1
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16	91	9.8	1815	3	US-09-327-925-1
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ALIGNMENTS

RESULT 1

US-09-422-869-21
; Sequence 21, Application US/09422869

; Patent No. 6235481

; GENERAL INFORMATION:

; APPLICANT: POLONSKY, KENNETH S.

; APPLICANT: HORIKAWA, YUKIO

; APPLICANT: ODA, NAOHISA

; APPLICANT: COX, NANCY J.

; APPLICANT: SREENAN, SEAMUS

; APPLICANT: ZHOU, YUN-PING

; APPLICANT: OTANI, KENICHI

; APPLICANT: HANIS, CRAIG L.

; APPLICANT: BELG, GRAEME I.

; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES

; FILE REFERENCE: ARCD:307

; CURRENT APPLICATION NUMBER: US/09/422,869

; CURRENT FILING DATE: 1999-10-21

; EARLIER APPLICATION NUMBER: 60/134,175

; EARLIER FILING DATE: 1999-05-13

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 21

; LENGTH: 1875

; TYPE: DNA

; ORGANISM: Human

US-09-422-869-21

Query Match 99.0%; Score 920.4; DB 3; Length 1875;
Best Local Similarity 99.4%; Pred. No. 2e+186;
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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; Patent No. 6235481
; GENERAL INFORMATION:
; APPLICANT: POLONSKY, KENNETH S.
; APPLICANT: HORIKAWA, YUKIO
; APPLICANT: ODA, NAOHISA
; APPLICANT: COX, NANCY J.
; APPLICANT: SREENAN, SEAMUS
; APPLICANT: ZHOU YUN-PING
; APPLICANT: OTANI, KENICHI
; APPLICANT: HANIS, CRAIG L.
; APPLICANT: BELL, GRAEME I.
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
; FILE REFERENCE: ARCD:307
; CURRENT APPLICATION NUMBER: US/09/422,869
; EARLIER FILING DATE: 1999-10-21
; EARLIER APPLICATION NUMBER: 60/134,175
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
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; LENGTH: 49136
; TYPE: DNA
; ORGANISM: Human
; US-09-422-869-1
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Query Match 99.0%; Score 920.4; DB 3; Length 49136;
Best Local Similarity 99.4%; Pred. No. 3.4e-186;
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-

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; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-3

Query Match      12.0%; Score 111.2; DB 3; Length 1089;
Best Local Similarity 50.3%; Pred. No. 1.4e-14;
Matches 309; Conservative 0; Mismatches 293; Indels 12; Gaps 1;

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QY 266 GCAGAGCTCTCCAGGGCATCTACTGACCAACAGGTATCATGAGCATCAGCTGGTCA 325
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Db CGGCGCGCTTCCATGACGAGCTCTTCCGAGACCGCTTACACCACTTCTGTGCTTG 508

QY 506 ATTTCAACTCCATGCGGTTCCCGTGTGGGATTTCTACTGCGCCCTGGCGGCTGGTGT 565
Db AGAAGTTCCCATGGAAGGTGGGTGGCTGCGTGAACCTCTATCGGCTTCTGTGGCT 568

QY 566 TCTGCTCCCTGAAGGTGGTACTGCGCTGCGGCGGAGGCGGCAACCGAGGTGGGCGG 625
Db TCTCTTCCGTGGCGCTCATGCTGCTGTGTCAGCGGGGCACTCTGCGGCGCGTGGGG 628

QY 626 CAGAGGCAACCGCAAGGCTAAACGATGTTCTGGGCGCAACCTCTGCTGTTCTGTTCT 685
Db GCAGCGTGTCCACCGAGCGCCAGGAGAGGCAAGATCAAGCGGCTGGCGCTCAGCCTCA 688

QY 686 GCTTCTGCGCCCTG 699
Db TCGCCATCGTGTGCTG 702

RESULT 6
US-09-016-434-1429
; Sequence 1429, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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QY 686 GCTTCTGCCCCCTG 699
Db 905 TCGCATCGTCTG 918

RESULT 7

US-09-850-948-1
; Sequence 1, Application US/09850948
; Patent No. 6919176
; GENERAL INFORMATION:
; APPLICANT: Yang, Jianxin
; APPLICANT: An, Songzhu
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Associated With Cancer
; FILE REFERENCE: 019781-008300US
; CURRENT APPLICATION NUMBER: US/09/850,948
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2693
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor 4 (GPR4)
; NAME/KEY: CDS
; LOCATION: (594)..(1682)
; OTHER INFORMATION: human G-protein coupled receptor 4 (GPR4)
US-09-850-948-1

Query Match 12.0%; Score 111.2; DB 3; Length 2693;

Best Local Similarity 50.3%; Pred. No. 1.6e-14; Mismatches 293; Indels 12; Gaps 1;
Matches 309; Conservative 0;

QY 98 TAGGCTGCTGCTCAACAGCTGGCGCTCTTGTCTGCGCGCATGACGAGTGGGA 157
Db 682 TGGGGTGGCCCAACTGCTGCTCTGTGGCGGCTACCGCCAGGTGCAACAGCGCA 741
QY 158 CGGAGACCGCGATATACATGACCAACTGGGGTGGCGACCTCTGCGCTGTGTGACCT 217
Db 742 ACGAGCTGGCGCTTACCTGATGAACCTCAGCATGCGCGACCTGTGTACATCTGACGCG 801
QY 218 TGGCTTGTGTGCTACTCCCTGCGAGAC-----ACCTCAGACGCGCGTGT 265
Db 802 TGGCGCTGTGGTGGACTACTTCTGCAACCACTGGATCCAGGCGCCCGGTCTCT 861
QY 266 GCGAGCTCTCCAGGCGCATCTACCTGACCAAGGTATACATGAGCATGAGCTGTGCAAGG 325
Db 862 GCAAGCTCTTGGGTTCATCTTCTACACCAATATCTACATGAGCATGCGCTTCTGTGCT 921
QY 326 CCATCGCGGTGACCGCTATGTGGCGGTGGCGACCGCGTGGCGCGCGCGGTGCGGT 385
Db 922 GCATCTCGGTGACCGCTACCTGGCTGTGGCGCCACCACTCGCTTGGCGCGCTGCGCC 981
QY 386 CCCCCAGGAGGCTGGCGCGGTGGCGCGGTCTCTGGGTGTGTGTATCGGCTTCTCTGG 445
Db 982 GCGTCAAGACCCGCGTGGCGGTGAGCTCCGTGTGGTCTGGGCCACGAGCTGGGCGCAACT 1041
QY 446 TGGCTGCTGCTCTCGGGATTCAGGAGGCGGCTTCTGCTTTCAGGAGCACCCGCGACA 505
Db 1042 CGGCGCCCTGTTCATGATGAGAGCTTCCGAGACCGCTTACCAACACACTTCTGTGTTG 1101
QY 506 ATTTCAACTCCATGCGGTTCCCGCTGCTGGGATTTCTACCTGCGCTTGGCGCGGTGGTCT 565
Db 1102 AGAAGTTCCCATGGAAGGCTGGGTGGCTGGATGAACCTCTATCGGGTGTTCGTGGGT 1161
QY 566 TCTGCTCTGAAAGTGTGTGACTGCGCTGGCGCCAGAGGCCACCCAGCAGTGGGGCAGG 625
Db 1162 TCTCTTCCGTTGGGCGCTCATGTCTGTCTGCTACCGGGGACATCTCTGCGGCGCGTGGG 1221
QY 626 CAGAGGCCACCCGAGGCTTAACGCAATGCTCTGGGCGCAACTCTCTGTGGTCTGCTGTCT 685

Db 1222 GCAGCGTGTCCACGAGCGCCAGGAGAACGCAAGATCAAGCGGCTGGCCCTCAGCCTCA 1281
QY 686 GCTTCTGCCCCCTG 699
Db 1282 TCGCATCGTCTG 1295

RESULT 8

US-09-170-496D-117
; Sequence 117, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-117

Query Match 11.8%; Score 110; DB 3; Length 1098;

Best Local Similarity 50.2%; Pred. No. 2.4e-14;
Matches 402; Conservative 0; Mismatches 365; Indels 33; Gaps 4;

QY 87 CCTGCTGTGTAGCGCTGTGCTCAACAGCTGGCGCTCTGGGTGTCTGTGCGCGCAT 146
Db 90 CGTGTGTGTGTGGCTTCCCGGCAACTGCTGTCTCTACTTGGCTACTGTCAGAT 149
QY 147 GCAGCAGTGGACGGAGACCCGCATCTACATGACCAACTGTGGGTGGCGGACCTTGTGCT 206
Db 150 CAAGCCCGGAACGAGCTGGGCGTGTACTGTGCAACCTGACGCTGGCGGACCTCTTCTA 209
QY 207 GCTGTGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 266
Db 210 CATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 269
QY 267 CCAGCTCTCCAGGCGCATCTACTGACC-----AACAGGTATACATGAGCATCAG 314
Db 270 GCAGCTGTCTGCGCAGGTGTGGGCTCTCTCTGTACGAGAACATCTATCATCAGCGTGG 329
QY 315 CTTGTCTACGCGCATTCGCGCGGCGCTATGTGGCGCTGCGGCGACCGCTGCTGCGCGG 374
Db 330 CTTCTCTGTGCTGCTTCCGTTGGACCGCTACTGCTGTGGCGCATCCCTTCCGCTTCCA 389
QY 375 CGGGCTGCGGTCTCCCGAGGAGGTGCGGCGGTGTGCGGCTGCTCTCTGGG-----T 425
Db 390 CCAGTTCCGAGCCCTTGAAGGCGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 449
QY 426 GCTGTGCTATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 485
Db 450 GCTTACCGAGCATCTACTTCTGATGACGAGAGGTCTATCGAGGAGGAGAACAGCAGCG 509
QY 486 CTTTACGAGACACCCCGGCAAAATTTCAAATCTCAATGCGGTTTCCGCTGCTGGGATTTACT 545
Db 510 GGTGTCTTTGAGCACTACCCCATCCAGGCGATGCGAGCGGCGCATCAACTACTACGCTT 569
QY 546 GCGGCTGCGGCGGTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 605
Db 570 CTTGTGTGGCTTCTCTTCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 629
QY 606 ACC-----ACCGAGGTGGGCGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 656
Db 630 CGCGCTGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 689
QY 657 CTGGGCGCAACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716

Query Match 11.8%; Score 110; DB 2; Length 1597;
Best Local Similarity 50.2%; Pred. No. 2.6e-14;
Matches 402; Conservative 0; Mismatches 365; Indels 33; Gaps 4;

QY 87 CCTGCTGCTAGGCTGTCTCAACAGAGCTTGGGCTGTGGTGTCTGCTGCCGAT 146
DB 431 CGTCTGGTGGGCTTCCGGCCAACTGCTGCTCTTCTACTTCCGCTACCTGCAGAT 490

QY 147 GCAGAGTGGACGAGAGCCCGCATCTCATGACCAACTGGCGGTGGCGGACCTTGCT 206
DB 491 CAAGGCCGGAACAGAGCTGGGCGTGTACTGTGCAACCTGACGGTGGCGGACCTTCTTA 550

QY 207 GCTGTGACCTTCCCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 266
DB 551 CATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 610

QY 267 CCAGCTCTCCAGGCGCATCTACCTGACC-----AACAGGTATCATGAGCATCAG 314
DB 611 CGACTGTCTGCGCAGGTGTGGGATCTCTCTGTACGAGAATCTATCATCAGGTGG 670

QY 315 CCTGCTACGCGCATTCGCGGTGGACCGCTATGTGGCCGTGGCGCAACCGCTGGCGCG 374
DB 671 CTCTCTGCTGCTATCTCCGTGGACCGCTACTGCTGCTGCTGCTGCTGCTGCTGCTG 730

QY 375 CGGCTGCGTCCCGCAGGAGGCTGCGCGGTGGTGGCGGTCTCTGCTGCTGCTGCTGCT 425
DB 731 CCAGTTCGCGAACCTGAAAGGCGCGCTGCGCGGTGACGCTGCTGCTGCTGCTGCTG 790

QY 426 GCTGTGATCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 485
DB 791 GCTGATCAGCATCTACTTCTGATGCAAGAGAGTCTATCGAGGACGAGAACGACCG 850

QY 486 CTTGAGGAGCACCAGGCAAAATTTCAACTCCATGCGGTTCGCGTGTGGGATTTACTCT 545
DB 851 CGTGTGCTTTGAGCATCTACCCCATCCAGCATGGCAGCGCGCATCAACTACTACCGCT 910

QY 546 GCCCTGCGCGGTGGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 605
DB 911 CTTGCTGCGCTTCTCTTCTCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 970

QY 606 ACCC-----ACCGAGTGGGCGAGGAGGCGCCAGGCTAAACGCTGCT 656
DB 971 CGCGTGGCGCGGAGCCAGCGCACCCAGAGAGCCGCAAGACAGATCCAGCGCTGCT 1030

QY 657 CTGGGCAACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716
DB 1031 GCTGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1090

QY 717 GCGCTCGAGTGGGCTGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 776
DB 1091 GCGCAGC---GTCTGGAGGCGAGCTGCGACTTCGCAAGGCGCTTTTCAACGCTTACA 1147

QY 777 CATACGAGCAGCTCTCAGATGCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 836
DB 1148 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1207

QY 837 GCGCAAGGAGTTCCAGGAGG 856
DB 1208 CAGCGAGACCAACCCAGCGG 1227

RESULT 11
US-09-364-425B-26
; Sequence 26, Application US/09364425B
; Patent No. 6653086
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Chen, Ruoping

; TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Receptor
; FILE REFERENCE: Aren0047
; CURRENT APPLICATION NUMBER: US/09/364,425B
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/094,879
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/106,300
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/110,906
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 1697
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-364-425B-26

Query Match 11.8%; Score 110; DB 3; Length 1697;
Best Local Similarity 50.2%; Pred. No. 2.6e-14;
Matches 402; Conservative 0; Mismatches 365; Indels 33; Gaps 4;

QY 87 CCTGCTGCTAGGCTGTCTCAACAGAGCTTGGGCTGTGGGCTGTCTGCTGCCGAT 146
DB 413 CGTCTGGTGGGCTTCCGGCCAACTGCTGCTCTTCTACTTGGGCTACCTGCAGAT 472

QY 147 GCAGAGTGGACGAGAGCCCGCATCTCATGACCAACTGGCGGTGGCGGACCTTGCT 206
DB 473 CAAGGCCGGAACAGAGCTGGGCGTGTACTGTGCAACCTGACGGTGGCGGACCTTCTTA 532

QY 207 GCTGTGACCTTCCCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 266
DB 533 CATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592

QY 267 CCAGCTCTCCAGGCGCATCTACCTGACC-----AACAGGTATCATGAGCATCAG 314
DB 593 CGACTGTCTGCGCAGGTGTGGGATCTCTCTGTACGAGAATCTATCATCAGGTGG 652

QY 315 CTTGCTACGCGCATTCGCGGTGGACCGCTATGTGGCCGTGGCGCAACCGCTGCGTGG 374
DB 653 CTCTCTGCTGCTATCTCCGTGGACCGCTACTGCTGCTGCTGCTGCTGCTGCTGCTG 712

QY 375 GCGCTGCGGTTCCTCCAGGAGGCTGCGCGGTGGTGGCGGTCTCTGCTGCTGCTGCT 425
DB 713 CCAGTTCGGAACCTTGAAGGCGCGCTGCGCGTTCAGCGTGGTCTATCTGGGCGCAAGAGCT 772

QY 426 GCTGTGATCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 485
DB 773 GCTGACGAGCATCTACTTCTGTATGACAGAGAGTCTATCGAGGACGAGAACGACGAC 832

QY 486 CTTGAGGAGCACCAGGCAAAATTTCAACTCCATGCGGTTCGCGTGTGGGATTTACTCT 545
DB 833 CGTGTGCTTTGAGCATCTACCCCATCCAGGATGGCAGCGCGCATCAACTACTACCGCTT 892

QY 546 GCCCTGCGCGGTGGTGTCTTCTGCTCTCTGAAAGTGGTGTGCTGCTGCTGCTGCTGCTG 605
DB 893 CTTGCTGCGGCTTCTCTCTTCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 952

QY 606 ACCC-----ACCGAGTGGGCGAGGAGGCGCCAGGCTAAACGCTGCTGCTGCTGCT 656
DB 953 CGCGCTGCGCGGAGCCAGGCAACGAGAGCGCGAGGACGAGATCCAGGCGCTGCT 1012

QY 657 CTGGGCAACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716
DB 1013 GCTGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1072

QY 717 GCGCTCGAGTGGGCTGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 776
DB 1073 GCGCAGC---GTCTGGGAGGCGAGCTGCGACTTCGCAAGGCGGCTTTTCAACGCTTACA 1129

QY 777 CATACGAGCAGCTCTCAGATGCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 836

Db 1130 CTTCTCCTCTGCTCAACAGCTTTCAATGCTGCGACGCCCTGCTCTACTGTTCTG 1189

Qy 837 GGCCAAGGAGTTCCAGGAGG 856

Db 1190 CAGCGAGACCAACCCACCGGG 1209

RESULT 12

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US-09-170-496D-165
; Sequence 165, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6553339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-165

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Query Match	11.8%	Score 109.6;	DB 3;	Length 1089;
Best Local Similarity	52.5%	Pred. No. 3e-14;		
Matches 272;	Conservative	0;	Mismatches 234;	Indels 12; Gaps 1;

98	Qy	TAGCCTGCTGCTCAA	CAGCGTGGCGTCTGGGGTTC	CTGCTGCCGATG	CAGCAGTGGA	157
89	Db	TGGGGCTGGCCACCAA	CTGCTGGTGGGGCGGCTA	CCGCCAGGTG	CAACAGCGCA	148
158	Qy	CGGAGACCCGCACTT	CATGACCAACTGGCGGTGGCGACCT	CTGCTGCTGTGCACCT	217	
149	Db	ACGAGCTGGGGCGTCT	CTGATGAACCTCAGCATCGCCGACCTGCT	GTACATCTGCACGC	208	
218	Qy	TGCCCTTCGTGTGCACT	CCCTCGCGAGAC-----	ACCTCAGACACGCGCGTGT	265	
209	Db	TGCGCTGTGGTGGACT	CTCTCTGCACACAGCAAACTGGATCCA	CGGCCCGGGTCTCT	268	
266	Qy	GCCAGCTCTCCCGAGGC	CACTACTCTGACCAACAGGTACTAGAGCAT	CAGCCTGTGCACGG	325	
269	Db	GCAAGCTCTTTGGGTT	CATCTTCTACACCAATATCTACATCAGCAT	CGCCTTCTCTGTGCT	328	
326	Qy	CGATGGCGGTGAGACG	CTATGTGGCCGTGGCGCAACCGCTGCCTG	CGCGGGCTGCGGT	385	
329	Db	GCATCTCGTGGGACCG	CTACTGGCTGTGGCCACCCCACTCGCTT	CGCCGCGCTGCGCC	388	
386	Qy	CCCCCAGCAGGCTGCG	CGCGCTGTGCGGGTCTCTCTGGGTGCTGGT	CATCGGTCCTCTGG	445	
389	Db	GCGTCAAGACCGCGT	GGCGCGTGAAGTCCGTGGTCTGGGCGCA	CGAGCTGGGGCCCAACT	448	
446	Qy	TGGCTCGCTGGCTCT	CTCGGGGATTCAAGAGGCGCGCTTCTGCTT	CAGAGACACCGGCACA	505	
449	Db	CGGGCCCCCTGTTC	CCATGAAGAGTCTTCGAGAACCGCTTAC	CAACCAACCTTCTGTCTTG	508	
506	Qy	ATTTCAACTCCATG	CGGTTC	CCGCTGTGGGATTTCTACCTGCCCTT	CGCGTGGTGGTCT	565
509	Db	AGAAGTTCCCACTGA	AGAGGCTGGGTGGCTGGATGAACCTCT	ATCGGGTGTTCGTGGGCT	568	
566	Qy	TCGTCTCCCTGAAG	TGGTGA	CTGACCTGGCCCTGGCCCGAGGG	603	
569	Db	TCCTCTTTCCGTGGG	CGCTCATGCTGTGTGCTGTCGTACCGG	606		

RESULT 13
US-09-170-496D-193
/ Sequence 193, Application US/09170496D

Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 193
LENGTH: 1128
TYPE: DNA
ORGANISM: Homo sapiens
US-09-170-496D-193

	Query Match	10.0%;	Score 92.6;	DB 3;	Length 1128;
	Best Local Similarity	47.9%;	Pred. No. 1.2e-10;		
	Matches	371;	Conservative	0;	Mismatches 389; Indels 15; Gaps 3;
Qy	66	CTTCTACGCTACTTGGGCGTCTCTGTGGTGTAGGCTCTGTCTCAACAGCCTGGCGCT	125		
Db	183	CTGGTGCTCTTACACCAATCTCTCTTCCCATCGGCTTTGTGGCAACATCCTGTATCCT	242		
Qy	126	CTGGGTGTTTCTGTGTCGCGCATGCAAGCAGTGGACGGAGACCGCATCTACATGACCAACT	185		
Db	243	GTTGGTGAAATCATCAGCTTCCGCGAGAAGATGACCATCCCGAGCTGTACTTCATCAACT	302		
Qy	186	GGCGTGGCGCACTCTGGCTCTGTGTGCACTTTGGCCCTTCGTGTGTGCACTCCCT--	239		
Db	303	GGCGTGGCGGACCTCATCTCTGTGGCGGACTCCCTCATTTAGAGTGTTCACCTTGCA	362		
Qy	240	GCGAGACACTCAGACACGCGCTGTGCCAGCTCTCCAGGGCATCTACCTGACCAACAG	299		
Db	363	GCGGTACTAGCAATCGCGCTCTGTGTGCACTTCTATGTGCTCTTCTGTGAGGTCAACAT	422		
Qy	300	GTACATGAGCATCAGCTGTGTCAAGGCGCATCGCGTGGACCGCTATGTGGCGTGGCA	359		
Db	423	GTACAGCAGCGTCTTCTTCTCCTGATGAGCTTCGACCGCTACATCGCCTGGCCAG	482		
Qy	360	CCGCTCGTGGCCGGGCTGCGGTCCCGAGGAGGCTGCGCCGTGTGTGCGGCTCTCT	419		
Db	483	GGCCATGCGTGCAGCGCTGTTCCGCAACCAAGCACACGCCCGGTGAGCTGTGGCCTCAT	542		
Qy	420	CTGGGTCTGGTCATCGGCTCCCTGGTGGCTCGCTGTGCTCTCTGGGATTCAGAGAGCGG	479		
Db	543	CTGGATGGCATCGTGTGCAGCAAGTGTGGTGGCTTTCACCGCGGTGCACCTGTGAGACAC	602		
Qy	480	CTTCTGTCTCAGAGACACCGGCACAAATTCATCTCCATCGGTTCCCGC-----TGCT	533		
Db	603	CGACGAGCGTGTCTTGTTTTCGGGATGTCCGGAGGTGCAGTGGCTCGAGGTCACGCT	662		
Qy	534	GGGATTTCACTGCCCTCTGGCCGTGGTGTCTTCTGTCTCCCTGAGAGTGGTGTGCTG	593		
Db	663	GGGCTTTCATGTGCCCTTTCGCCATCATCGGCCCTGTGTCTATCTCCCTCATTTGTTCGGGGTGT	722		
Qy	594	GGGCCAGAGGCCACCAACCGACCGTGGGGCAGGACAGAGGCCACCGCAAGGTCTAAACGCAT	653		
Db	723	GGTC--AGGGCGCACCGGCACCGTGGCTGCGGCCCGCGGCGAGAGGGGAAACGCAT	779		
Qy	654	GGTCTGGGCGCAACTCTGTGTGTGTGTGTGTCTTCTGTCTCCCTGAGAGTGGTGTGCTG	713		
Db	780	GATCTCTCGCGGTGGTGTGTGTCTTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	839		
Qy	714	AGTGGCTCTGCAGTGGGCTGGGAAGCGCTCTGTGCCCTCTCTGGAGACGATCCGTGCGGCTCT	773		
Db	840	CGTGCACTCTGTGACGGGACGAGCGCTGGGGCGGCTCTCTGTGACGAGCATGTCTTTCGCGCA	899		
Qy	774	GTACATAACAGCAAGCTCTCAGATGCCAACTGTCTGTCTGGAGCGCCATCTGTCTAC	828		
Db	900	TGCCCACTTCTCAGCGGCGCACATTTGCAACCTCGCGGCTTCTTCCCAACAGCTGC	954		

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OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 06:08:01 ; Search time 947 Seconds
(without alignments)

8120.931 Million cell updates/sec

Title: US-10-083-168-84

Perfect score: 930

Sequence: 1 atgaatggcaccctacaacac.....tgtgctgaccctgcctaa 930

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	925.2	99.5	930	5	US-10-225-567A-491
4	925.2	99.5	930	5	US-10-696-639-6
5	920.4	99.0	1875	3	US-09-768-877-21
6	920.4	99.0	1875	3	US-10-157-031-350
7	920.4	99.0	49136	3	US-09-768-877-1
8	919	98.8	1644	9	US-10-505-486-186
9	916.8	98.6	24477	8	US-10-741-600-17827
10	900	96.8	1989	6	US-10-101-510-636
11	439.2	47.2	600	10	US-11-060-756-1687
12	439.2	47.2	600	10	US-11-060-756-5959
13	200.6	21.6	201	8	US-10-741-600-61537
14	200.6	21.6	201	8	US-10-741-600-61547
15	200.6	21.6	201	8	US-10-741-600-61549
16	200.6	21.6	201	8	US-10-741-600-61551
17	200.6	21.6	201	8	US-10-741-600-61552
18	200.6	21.6	201	8	US-10-741-600-61567
19	200.6	21.6	201	8	US-10-741-600-61568
20	197.4	21.2	201	8	US-10-741-600-61525
21	197.4	21.2	201	8	US-10-741-600-61532
22	197.4	21.2	201	8	US-10-741-600-61535
23	195.8	21.1	201	8	US-10-741-600-61565

24	172.6	18.6	201	8	US-10-741-600-61546	Sequence 61546, A
25	150.6	16.2	201	8	US-10-741-600-61524	Sequence 61524, A
26	141.8	15.2	1854	3	US-09-866-050A-596	Sequence 596, App
27	141.8	15.2	1854	5	US-10-152-661-596	Sequence 596, App
28	111.6	12.0	1098	5	US-10-251-385-225	Sequence 225, App
29	111.2	12.0	1089	5	US-10-251-385-3	Sequence 3, Appli
30	111.2	12.0	1089	5	US-10-267-811-1	Sequence 1, Appli
31	111.2	12.0	1089	5	US-10-101-510-17	Sequence 17, Appli
32	111.2	12.0	1365	6	US-10-305-720-1429	Sequence 1429, Ap
33	111.2	12.0	1365	7	US-10-283-975A-113	Sequence 113, App
34	111.2	12.0	2693	3	US-09-850-948-1	Sequence 1, Appli
35	111.2	12.0	2693	3	US-10-273-575-1	Sequence 1, Appli
36	111.2	12.0	2696	5	US-10-225-567A-272	Sequence 272, App
37	111.2	12.0	2696	7	US-10-712-124-113	Sequence 113, App
38	111.2	12.0	2980	6	US-10-101-510-456	Sequence 456, App
39	110.4	11.9	1149	9	US-10-450-763-23834	Sequence 23834, A
40	110.4	11.9	1617	5	US-10-167-192-2	Sequence 2, Appli
41	110.4	11.9	1617	5	US-10-400-991-5	Sequence 5, Appli
42	110.4	11.9	1674	9	US-10-505-486-147	Sequence 147, App
43	110	11.8	1098	3	US-09-850-948-5	Sequence 5, Appli
44	110	11.8	1098	5	US-10-251-385-117	Sequence 117, App
45	110	11.8	1098	5	US-10-273-575-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-10-083-168-84
; Sequence 84, Application US/10083168
; Publication No. US20030023069A1

GENERAL INFORMATION:

APPLICANT: Liaw, Chen W.
APPLICANT: Chalmers, Derek T.
APPLICANT: Behan, Dominic P.
APPLICANT: Maciejewski-Lenior, Dominique
APPLICANT: Leonard, James N.
APPLICANT: Ortuno, Daniel
APPLICANT: Lin, I-Lin

TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Act

TITLE OF INVENTION: Receptors

FILE REFERENCE: AREN-0320

CURRENT APPLICATION NUMBER: US/10/083.168

CURRENT FILING DATE: 2002-02-26

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PatentIn version 3.1

SEQ ID NO 84

LENGTH: 930

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: No. US20030023069A1el Sequence

US-10-083-168-84

Query Match 100.0%; Score 930; DB 5; Length 930;

Best Local Similarity 100.0%; Pred. No. 2.6e-225;

Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAATGGCACCCTACAACACCTGTGGCTCCAGCGACCTCAGCTGGCCCCCAGGATCAAG	60
Db	1	ATGAATGGCACCCTACAACACCTGTGGCTCCAGCGACCTCAGCTGGCCCCCAGGATCAAG	60
Qy	61	CTGGGCTTCTAGCCCTACTTGGCGCTGCTGGTGTAGGCTTGTCTCAACGCTG	120
Db	61	CTGGGCTTCTAGCCCTACTTGGCGCTGCTGGTGTAGGCTTGTCTCAACGCTG	120
Qy	121	GGCTCTGGGTCTTCTGCTGCGCATGCGAGTGGAGCGAGACCGGCACTTACATGACC	180
Db	121	GGCTCTGGGTCTTCTGCTGCGCATGCGAGTGGAGCGAGACCGGCACTTACATGACC	180
Qy	181	AACTGGCGGTGGCGACCTTGTGCTGTGTGCACTTGGCCCTTGTGTGCACTCCCTG	240
Db	181	AACTGGCGGTGGCGACCTTGTGCTGTGTGCACTTGGCCCTTGTGTGCACTCCCTG	240

Sequence 491, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 232
SOFTWARE: PatentIn version 3.1
SEQ ID NO 491
LENGTH: 930
TYPE: DNA
ORGANISM: Homo sapiens
US-10-225-567A-491

Query Match 99.5%; Score 925.2; DB 5; Length 930;
Best Local Similarity 99.7%; Pred. No. 4.3e-224;
Matches 927; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGAATGGCACCTACACACACTGGCTCCAGGACCTCACCTGGCCCCCAGCGATCAAG 60
Db |||
Qy 1 ATGAATGGCACCTACACACACTGGCTCCAGGACCTCACCTGGCCCCCAGCGATCAAG 60
Db |||
Qy 61 CTGGGCTTCTACGGCTACTCTGGGGCTCTCTGCTGGTGTAGGCCCTGCTGCTCAACAGCGTG 120
Db |||
Qy 61 CTGGGCTTCTACGGCTACTCTGGGGCTCTCTGCTGGTGTAGGCCCTGCTGCTCAACAGCGTG 120
Db |||
Qy 121 GCGCTCTGGGTGTTCTGTCGCCGATGACAGTCAGTCAGTGGAGAGCCCGATCTCATGACCC 180
Db |||
Qy 121 GCGCTCTGGGTGTTCTGTCGCCGATGACAGTCAGTCAGTGGAGAGCCCGATCTCATGACCC 180
Db |||
Qy 181 AACCTGGGGTGGCGGACCTCTGGCTGTGTGGTGGCACTTGGCTTGGCTGCTGCTGCTGCTG 240
Db |||
Qy 181 AACCTGGGGTGGCGGACCTCTGGCTGTGTGGTGGCACTTGGCTTGGCTGCTGCTGCTGCTG 240
Db |||
Qy 241 CGAGACACTCAGACACCGCGCTGTGCCAGCTCTCCAGGGCATCTACTTGACCAACAGG 300
Db |||
Qy 241 CGAGACACTCAGACACCGCGCTGTGCCAGCTCTCCAGGGCATCTACTTGACCAACAGG 300
Db |||
Qy 301 TACATGAGCATCAGCTGGTCAACCGCCATGCGCGGTGACCGGTATGTCGGCCGTGGGGAC 360
Db |||
Qy 301 TACATGAGCATCAGCTGGTCAACCGCCATGCGCGGTGACCGGTATGTCGGCCGTGGGGAC 360
Db |||
Qy 361 CGCTGCGTGCCTGGCGGGCTGGGTCCCGCAGGAGGCTGGCGCGTGTGCGCGTCTCTC 420
Db |||
Qy 361 CGCTGCGTGCCTGGCGGGCTGGGTCCCGCAGGAGGCTGGCGCGTGTGCGCGTCTCTC 420
Db |||
Qy 421 TGGGTGCTGGTTCATCGGCTCCCTGGTGGCTCGCTGGCTCCTGGGGATTTCAGGAGGGCGG 480
Db |||
Qy 421 TGGGTGCTGGTTCATCGGCTCCCTGGTGGCTCGCTGGCTCCTGGGGATTTCAGGAGGGCGG 480
Db |||
Qy 481 TTCTGCTTCAGGAGACCCGGGCAATTTCAATCCATGCGGTTCGCCCTGCTGGATTC 540
Db |||
Qy 481 TTCTGCTTCAGGAGACCCGGGCAATTTCAATCCATGCGGTTCGCCCTGCTGGATTC 540
Db |||
Qy 541 TACCTGCCCTCGGCGGTGGTGTCTTCTGCTCCCTGAAAGTGGTGACTGCCCTGGCCCGAG 600
Db |||
Qy 541 TACCTGCCCTCGGCGGTGGTGTCTTCTGCTCCCTGAAAGTGGTGACTGCCCTGGCCCGAG 600
Db |||
Qy 601 AGGCCACCCACCGAGCTGGGGCAGGACAGGGCCACCCGCAAGGCTTAAACGCAATGCTGG 660
Db |||
Qy 601 AGGCCACCCACCGAGCTGGGGCAGGACAGGGCCACCCGCAAGGCTTAAACGCAATGCTGG 660
Db |||
Qy 661 GCCAACCTCTGGTGTGTGTCTGCTTCCTGCCCTGACGTCGGGGCTGACAGTGGCG 720
Db |||
Qy 661 GCCAACCTCTGGTGTGTGTGTCTGCTTCCTGCCCTGACGTCGGGGCTGACAGTGGCG 720
Db |||

:	NUMBER OF SEQ ID NOS:	415			
:	SOFTWARE:	PatentIn version 3.1			
:	SEQ ID NO	350			
:	LENGTH:	1875			
:	TYPE:	DNA			
:	ORGANISM:	Homo sapiens			
:	US-10-157-031-	350			
<hr/>					
	Query Match	99.0%;	Score 920.4;	DB 5;	Length 1875;
	Best Local Similarity	99.4%;	Pred. No. 7.1e-223;		
	Matches 924;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
<hr/>					
Qy	1	ATGAATGGCACCTTACAAACACTGTGGGCTTCAGCGCAGCTCACTTGCGGCCCCAGCGCATCAAG	60		
Db	576	ATGAATGGCACCTTACAAACACTGTGGGCTTCAGCGCAGCTCACTTGCGGCCCCAGCGCATCAAG	635		
<hr/>					
Qy	61	CTGGGCTTTACGCCTACTATTGGGGCTCTGCTGGTGTAGCGCTGTGCTCAAACGCCTG	120		
Db	636	CTGGGCTTTACGCCTACTATTGGGGCTCTGCTGGTGTAGCGCTGTGCTCAAACGCCTG	695		
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Qy	121	GCGCTCTGGGTGTTCTGCTGCGGATGCGAGTAGTGACGAGACCGCGCATCTACATGACC	180		
Db	696	GCGCTCTGGGTGTTCTGCTGCGGATGCGAGTAGTGACGAGACCGCGCATCTACATGACC	755		
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Qy	181	AACCTGGCGGTGGCGACCTCTGCTGCTGTGCACCTTGCCCTTCGTGCTGCACTCCCTG	240		
Db	756	AACCTGGCGGTGGCGACCTCTGCTGCTGTGCACCTTGCCCTTCGTGCTGCACTCCCTG	815		
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Qy	241	CGAGACACCTCAGACACGCGGCTGTGCGAGCTCTCCCAGGGGCATCTACCTGACCAACAGG	300		
Db	816	CGAGACACCTCAGACACGCGGCTGTGCGAGCTCTCCCAGGGGCATCTACCTGACCAACAGG	875		
<hr/>					
Qy	301	TACATGAGCATACGCCCTGGTCAOCCGCATATGCCGTGTGACCGCTATATGGCCGTGCGGCAC	360		
Db	876	TACATGAGCATACGCCCTGGTCAOCCGCATATGCCGTGTGACCGCTATATGGCCGTGCGGCAC	935		
<hr/>					
Qy	361	CCGCTGTGTGCCCCGGGGCTGGGTCCTCCCGACGAGCTGGGCGCGTGTGGCGGCTCCTC	420		
Db	936	CCGCTGTGTGCCCCGGGGCTGGGTCCTCCCGACGAGCTGGGCGCGTGTGGCGGCTCCTC	995		
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Qy	421	TGGGTGTGTGTCACTGGGCTCCTCGTGGCTCGCTGGGCTCTCTGGGGATTCACGAGGGCGGC	480		
Db	996	TGGGTGTGTGTCACTGGGCTCCTCGTGGGCTCGCTGGGCTCTCTGGGGATTCACGAGGGCGGC	1055		
<hr/>					
Qy	481	TTCTGCTTCAGGAGCACCCGCCACAATTTCAACTCCAATGCGGTTTCCCGCTGTGGGATTC	540		
Db	1056	TTCTGCTTCAGGAGCACCCGCCACAATTTCAACTCCAATGCGGTTTCCCGCTGTGGGATTC	1115		
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Qy	541	TACCTGCCCTTGCGCGTGGTGGTCTTCTGCTCCCTGAAGGTGTGACCTGCCCTGGCCCCAG	600		
Db	1116	TACCTGCCCTTGCGCGTGGTGGTCTTCTGCTCCCTGAAGGTGTGACCTGCCCTGGCCCCAG	1175		
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Qy	601	AGGCCACCCACGAGCTGGGGCAGSACAGSGCCACCCGCAAGGCTAAACGATCGTCTGG	660		
Db	1176	AGGCCACCCACGAGCTGGGGCAGSACAGSGCCACCCGCAAGGCTAAACGATCGTCTGG	1235		
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Qy	661	GCCAACTCTCTGGTGTTCGTGCTCTGCTTCTTGCCCTTGACGCTGGGGCTGACAGTGGC	720		
Db	1236	GCCAACTCTCTGGTGTTCGTGCTCTGCTTCTTGCCCTTGACGCTGGGGCTGACAGTGGC	1295		
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Qy	721	CTCGAGTGGGCTGAAAAGCCTGTGCGCTCTCTGAGAGAGATCCCGTGGCGCCCTGTACATA	780		
Db	1296	CTCGAGTGGGCTGAAAAGCCTGTGCGCTCTCTGAGAGAGATCCCGTGGCGCCCTGTACATA	1355		
<hr/>					
Qy	781	ACCAGAAGCTCTCAGATGCCAACCTGCTGCTGGAGCGGCATCTGCTACTACTACATGSCC	840		
Db	1356	ACCAGAAGCTCTCAGATGCCAACCTGCTGCTGGAGCGGCATCTGCTACTACTACATGSCC	1415		
<hr/>					
Qy	841	AAGGAGTTCCAGGAGCGCTGTGCACTGGCCGCTGGCTCCCCCGTGTAAAGGCCCCACAAAGC	900		
Db	1416	AAGGAGTTCCAGGAGCGCTGTGCACTGGCCGCTGGCTCCCCCGTGTAAAGGCCCCACAAAGC	1475		
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Qy	901	CAGGACTCTGTGTGGTGAACCTTCGCCATAA	930		


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Qy 61 CTGGGCTTCTACGCTACTTGGGCGTCTGCTGCTAGCCCTGCTGCTCAACAGGCTG 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17239 CTGGGCTTCTACRCTACTTGGGCGTCTGCTGCTAGCCCTGCTGCTCAACAGGCTG 17298
Qy 121 GCGCTCTGGGTGTTCTGCTGCGCATGAGCAGTGGACGGAGACCCGCTCATCATGACC 180
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17299 GCSCTCTGGGTGTTCTGCTGCGCATGAGCAGTGGACGGAGACCCGCTCATCATGACC 17358
Qy 181 AACCTGGCGGTGGCCGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17359 AACCTGGCGGTGGCCGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 17418
Qy 241 CGAGACACTCAGACAGCGCGCTGCGCAGCTCTCCAGGGCATCTACCTGACCAACAGG 300
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17419 CGAGACACTCAGACAGCGCGCTGCGCAGCTCTCCAGGGCATCTACCTGACCAACAGG 17478
Qy 301 TACATGAGCATCAGCCTGGTCAAGCCCATCCCGTGGACCGCTATGTGGCGTGGCGAC 360
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17479 TACATGAGCATCAGCCTGGTCAAGCCCATCCCGTGGACCGCTATGTGGCGTGGCGAC 17538
Qy 361 CCGCTGGGTGGCGGCGTGGGTGCGGTCGCCAGGAGGCTGGCGCGGTGGCGCGTCTC 420
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17539 CCGCTGGGTGGCGGCGTGGGTGCGGTCGCCAGGAGGCTGGCGCGGTGGCGCGTCTC 17598
Qy 421 TGGGTGCTGGTCAATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17599 TGGGTGCTGGTCAATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 17658
Qy 481 TTCTGCTTTCAGGAGACCCCGGCAAAATTTCAATCTCCATGCGGTTCCCGCTGCTGGATTC 540
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17659 TTCTGCTTTCAGGAGACCCCGGCAAAATTTCAATCTCCATGCGGTTCCCGCTGCTGGATTC 17718
Qy 541 TACTGCCCCCTGGCGGTGGTCTTCTGCTCCCTGAAAGTGGTGAATGCCCCCTGGCCGAG 600
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17719 TACTGCCCCCTGGCGGTGGTCTTCTGCTCCCTGAAAGTGGTGAATGCCCCCTGGCCGAG 17778
Qy 601 AGGCCACCCACGAGCTGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17779 AGGCCACCCACGAGCTGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 17838
Qy 661 GCCAACCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17839 GCCAACCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 17898
Qy 721 CTGCGAGTGGGTGGAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17899 CTGCGAGTGGGTGGAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 17958
Qy 781 ACCAGCAAGCTCTCAGATGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17959 ACCAGCAAGCTCTCAGATGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 18018
Qy 841 AAGGAGTTCAGAGGCGTCTGCACTGGCGCGTGGCTCCCGCTGCTGCTGCTGCTGCTGCT 900
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18019 AAGGAGTTCAGAGGCGTCTGCACTGGCGCGTGGCTCCCGCTGCTGCTGCTGCTGCTGCT 18078
Qy 901 CAGGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 930
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18079 CAGGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 18108
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RESULT 10
US-10-101-510-636
; Sequence 636, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20

; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 636
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1912)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1928)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-101-510-636

Query Match 96.8%; Score 900; DB 6; Length 1989;
Best Local Similarity 99.2%; Pred. No. 1e-217;
Matches 925; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
Qy 1 ATGATGGGACCTACACACCTGTGGCTCCAGGACCTCACCTGGCCCCCAGGCGATCAAG 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
214 ATGATGGGACCTACACACCTGTGGCTCCAGGACCTCACCTGGCCCCCAGGCGATCAAG 273
Qy 61 CTGGGCTTCTACGCTACTTGGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
274 CTGGGCTTCTACGCTACTTGGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 333
Qy 121 GCGCTCTGGGTGTTCTGCTGCGCATGAGCAGTGGACGGAGACCCGCTCATCATGACC 180
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
334 GCGCTCTGGGTGTTCTGCTGCGCATGAGCAGTGGACGGAGACCCGCTCATCATGACC 393
Qy 181 AACCTGGCGGTGGCCGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
394 AACCTGGCGGTGGCCGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 453
Qy 241 CGAGACA - CTTACAGACAGCGCTGTGCGACTCTCCAGGGCATCTACCTGACCAACAG 299
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
454 CGAGACAGCTTACAGACAGCGCGCTGTGCGACTCTCCAGGGCATCTACCTGACCAACAG 513
Qy 300 GTACATGAGCATCAGCCTGGTCAAGCGCATGCGCGTGGACCGCTATGTGGCGGTGGCGCA 359
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
514 GTACATGAGCATCAGCCTGGTCAAGCGCATGCGCGTGGACCGCTATGTGGCGGTGGCGCA 573
Qy 360 CCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 418
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
574 CCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 633
Qy 419 TCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 478
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
634 TCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 693
Qy 479 GCTTCTGCTTTCAGGAGCACCCGCGCAAAATTTCAACTCCATGCGGTTCGCTGCTGGGAT 538
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
694 GCTTCTGCTTTCAGGAGCACCCGCGCAAAATTTCAACTCCATGCGGTTCGCTGCTGGGAT 753
Qy 539 TCTACCTGCCCCCTGGCGCGTGGTGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 598
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
754 TCTACCTGCCCCCTGGCGCGTGGTGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813
Qy 599 AGAGGCCACCCACCGAGTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 658
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814 AGAGGCCACCCACCGAGTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 873
Qy 659 GGGCCAACTCTCTGGTGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 718
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
874 GGGCCAACTCTCTGGTGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 933
Qy 719 GCCTCGCAGTGGGTGGAAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 778
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
934 GCCTCGCAGTGGGTGGAAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 993


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Query Match      21.6%; Score 200.6; DB 8; Length 201;
Best Local Similarity 99.5%; Pred. No. 6.4e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 223 TTCTGTCTGCACTCCCTCGAGACACCTTCAGACACGCGGTGTGCTCCAGCTTCCAGGGC 282
Db 1 TTCTGTCTGCACTCCCTCGAGACACCTTCAGACACGCGGTGTGCTCCAGCTTCCAGGGC 60

Qy 283 ATCTACTGACCAACAGGTATCATGAGCATGAGCTGTGCTCAGGCGCATGCGGTGAGCGC 342
Db 61 ATCTACTGACCAACAGGTATCATGAGCATGAGCTGTGCTCAGGCGCATGCGGTGAGCGC 120

Qy 343 TATGTGCGCGGCGGACCGCTGCGTCCCGCGGCTCGGCTCCCGCAGGCTGCG 402
Db 121 TATGTGCGCGGCGGACCGCTGCGTCCCGCGGCTCGGCTCCCGCAGGCTGCG 180

Qy 403 GCCGTGTGCGGCTCTCTGG 423
Db 181 GCCGTGTGCGGCTCTCTGG 201

RESULT 14
US-10-741-600-61547
; Sequence 61547, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61547
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-741-600-61547

Query Match      21.6%; Score 200.6; DB 8; Length 201;
Best Local Similarity 99.5%; Pred. No. 6.4e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 23 GTGGCTCCAGGACCTCACTGGCCCCCAGCGCATCAAGCTGGCTTCTACGCTTACTTGG 82
Db 1 GTGGCTCCAGGACCTCACTGGCCCCCAGCGCATCAAGCTGGCTTCTACGCTTACTTGG 60

Qy 83 GCGTCTGTGTGTAGGCTGTGCTCAACAGCTGGCGCTCTGGGTGTTCTGTGCTGCC 142
Db 61 GCGTCTGTGTGTAGGCTGTGCTCAACAGCTGGCGCTCTGGGTGTTCTGTGCTGCC 120

Qy 143 GCATCAGCAGTGGAGCGGAGCCGCATCATGATCAACCACTGGCGGTGGCGACCTCT 202
Db 121 GCATCAGCAGTGGAGCGGAGCCGCATCATGATCAACCACTGGCGGTGGCGACCTCT 180

Qy 203 GCCTGTGTGACCTTGGCCCT 223
Db 181 GCCTGTGTGACCTTGGCCCT 201

RESULT 15
US-10-741-600-61549
; Sequence 61549, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
```

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; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61549
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-61549

Query Match      21.6%; Score 200.6; DB 8; Length 201;
Best Local Similarity 99.5%; Pred. No. 6.4e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 276 CCAGGGCATCTTACCTGACCAACAGGTATCATGAGCATCAGCTGTGTCAGGGCATCGCGT 335
Db 1 CCAGGGCATCTTACCTGACCAACAGGTATCATGAGCATCAGCTGTGTCAGGGCATCGCGT 60

Qy 336 GGACCGCTATGTGCGCGTGGCGCACCGCTCGGTGCGCGGCTGCGGTCCCCCAGGCA 395
Db 61 GGACCGCTATGTGCGCGTGGCGCACCGCTCGGTGCGCGGCTGCGGTCCCCCAGGCA 120

Qy 396 GGCTGCGGCGGTGTGCGCGGTCTCTGGGTCTGCTGCTCATCGGCTCCCTGTGGTCTGCTG 455
Db 121 GGCTGCGGCGGTGTGCGCGGTCTCTGGGTCTGCTGCTCATCGGCTCCCTGTGGTCTGCTG 180

Qy 456 GCTCTGCGGGATTTCAGGAGGG 476
Db 181 GCTCTGCGGGATTTCAGGAGGG 201
```

Search completed: February 11, 2006, 09:51:07
Job time : 948 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	110	11.8	1523	11	US-11-127-877-30	Sequence 30, Appl	
2	89	9.6	1238	7	US-10-995-561-321	Sequence 321, App	
3	89	9.6	1498	7	US-10-995-561-320	Sequence 320, App	
4	89	9.6	2095	7	US-10-750-185-61969	Sequence 61969, A	
5	89	9.6	2095	7	US-10-750-185-61969	Sequence 61969, A	
6	89	9.6	86131	7	US-10-995-561-13298	Sequence 13298, A	
C 7	88.2	9.5	1685	7	US-10-750-185-36071	Sequence 36071, A	
C 8	88.2	9.5	1685	7	US-10-750-623-36071	Sequence 36071, A	
9	84.2	9.1	1077	11	US-11-127-877-29	Sequence 29, Appl	
10	75.2	8.1	2011	11	US-11-136-527-3805	Sequence 3805, Ap	
C 11	74.2	8.0	706	7	US-10-750-185-32790	Sequence 32790, A	
C 12	74.2	8.0	706	7	US-10-750-623-32790	Sequence 32790, A	
13	73	7.8	1278	11	US-11-136-527-3310	Sequence 3310, Ap	
14	72.4	7.8	1428	7	US-10-995-561-28	Sequence 28, Appl	
15	72.4	7.8	13428	7	US-10-995-561-13208	Sequence 13208, A	
16	72.2	7.8	4267	11	US-11-127-877-15	Sequence 15, Appl	
17	71.8	7.7	2955	11	US-11-136-527-2954	Sequence 2954, Ap	
18	71.6	7.7	1290	11	US-11-136-527-2457	Sequence 2457, Ap	
19	71.6	7.7	1290	11	US-11-136-527-6553	Sequence 6553, Ap	
20	71	7.6	3023	11	US-11-127-877-22	Sequence 22, Appl	
21	71	7.6	3023	11	US-11-136-527-3778	Sequence 3778, Ap	

[illegible]

Db 610 CGACCTGTCTCTGCGAGGTGCGGCATCTCTCTGTACGAGAACATCTATCATCAGCGTGGG 669
Qy 315 CTGTGTACAGGCCATCGCGTGTGACCGCTATGTGGCGGTGCGGCACCGCTGGTGGCCGG 374
Db 670 CTTCCTCTGTGTGATCTCGGTGTGACCGCTACCTGGCTGTGGCCATCTCCCTTCGGCTTCCA 729
Qy 375 CGGGCTGGCGTCCCGCAGGCGAGCTGGCGCGGTGTCGGGGTCTCTGGG-----T 425
Db 730 CAGTTCGGAGCCCTGAGCGGCCCTCGCGGTGACGGGTGATCTGGGCCAAGAGCT 789
Qy 426 GCTGTGTATCGGCTCCCTGTGTGCTCGCTGGCTCTCTGGGATTTGAGAGGGCGGCTTTG 485
Db 790 GCTGACGAGCATCTCTCTGTATGACGAGGAGGTTCATCGAGGAGAGAGACGAGCACCG 849
Qy 486 CTTTACGAGGACCGCGGACAAATTTCAATCTCATGCGGTTCGCGCTCTCTGGGATTTTACT 545
Db 850 CGTGTGCTTTGAGCACTACCCCATCCAGGATGGCAGCGCGCCATCAACTACTACCGCTT 909
Qy 546 GCGCCTGGCGGTGGTCTCTGTCTCCCTGAAGGTGTGACTGCGCTGGCCCGAGAGCC 605
Db 910 CTRGTGGGCTTCCTCTTCCCATCTGCTGTCTGTGCGGTCTTACGAGGCACTCTGCG 969
Qy 606 ACCC-----ACCGAGTGGGGCAGGCGCAGAGGCCACCGCAAGGCTAAACGCAATGT 656
Db 970 GCGGTGGCGGAGCCACGGCACCGAGAGCGCGCAAGGACCATCCAGCGGTGT 1029
Qy 657 CTGGGCAACCTCTCTGGTGTGTGTCTGTCTCTGCTTCTGCGCTGCGCATCGTGGGCTGACGT 716
Db 1030 GCTCAGCAGCGTGTGTCTCTCTGCGCTCTCTCTGCGCTTACCGATGTGTGTGTGT 1089
Qy 717 GCGCTCGCAGTGGCTGGAAGCGCTGTGCGCTCTCTGGAGAGATCGGTGGCGCTGTGA 776
Db 1090 GCGCAGC---GTCTGGAGCGCAGCTGCGACTTTCGCAAGGGGTTTCAAGCGCTTACCA 1146
Qy 777 CATAACGAGCAAGCTCTCAGATGCCAACTGCTGCGGAGCGCATCTGCTACTACTACAT 836
Db 1147 CTCTCTCTCTGCTCAGCAGTTTCACTGCTGTGCGGAGCCCGTGTCTTACTGTCTGT 1206
Qy 837 GCGCAAGGAGTTCCAGAGG 856
Db 1207 CAGCGAGACCAACCGCGG 1226

RESULT 2
US-10-995-561-321
; Sequence 321, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-321

Query Match 9.6%; Score 89; DB 7; Length 1238;
Best Local Similarity 55.5%; Pred. No. 5e-09;
Matches 217; Conservative 0; Mismatches 165; Indels 9; Gaps 2;

Qy 45 GCGCCGAGGATCAAGCTGGGCTTCTACGCTACTTGGGGCTCTCTGCTGTGTAGGCT 104
Db 197 GCGGGCGGGGATGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 256
Qy 105 GCTGCTCAACAGCCTGGCGCTCTGGGTGTCTGTCTGCGCATGACGAGTGTGACGAGAC 164

Db 257 GGTGGGCGGCGGATCAAGCTGGGCTTCTACGCTACTTGGCGCTCTGTGTGTGTGTGTGT 104
Qy 197 GCGGGCGGGGATGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 256
Db 105 GCTGCTCAACAGCCTGGCGCTCTGGGTGTCTGTCTGCGCATGACGAGTGTGACGAGAC 164
Qy 257 GGTGGGCGGCGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 316
Db 165 CCGCATCTACATGACCAACCTGGCGGTGCGGACCTCTGTCTGTGTGTGTGTGTGTGTGTGT 224
Qy 317 CAMCATCTACCTGTCTCAACCTGGCGGTAGCGGAGCTCTTCACTGTGAGCGTGTGTGT 376
Db 225 CGT-----GCTGTCACTCCCTGGGAGAC---ACCTCAGACAGCGCGCTGTGTGTGTGT 275
Qy 377 CGTGGCCTGTGTCGCGCGCCCTGCGCCACTGCGCCCTTGGCTCCGTGTGTGTGTGTGTGT 436
Db 276 CCAGGGCATCTACCTGACCAACAGGTATACATGAGCATCAGCCTGTGTGTGTGTGTGTGT 335
Qy 437 GCTCAGCGTGTGAGCGGCTCAACATGTTTACCAGCGTCTTCTGTCTCACCGTGTGTGTGT 496
Db 336 GGAACGCTATGTGTGGCGGTGCGGACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 395
Qy 497 GGAACGCTACGTGTGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 556
Db 396 GGTGTGGCGCGGTGTGTGGCGGTCTCTGTGGTG 426
Qy 557 GGTGTGGCGGTGTGTGGCGGTGTGTGGTG 587

RESULT 3
US-10-995-561-320
; Sequence 320, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 320
; LENGTH: 1498
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-320

Query Match 9.6%; Score 89; DB 7; Length 1498;
Best Local Similarity 55.5%; Pred. No. 5.1e-09;
Matches 217; Conservative 0; Mismatches 165; Indels 9; Gaps 2;

Qy 45 GCGCCGAGGATCAAGCTGGGCTTCTACGCTACTTGGCGCTCTGTGTGTGTGTGTGTGTGT 104
Db 197 GCGGGCGGGGATGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 256
Qy 105 GCTGCTCAACAGCCTGGCGCTCTGGGTGTCTGTCTGCGCATGACGAGTGTGACGAGAC 164
Db 257 GGTGGGCGGCGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 316
Qy 165 CCGCATCTACATGACCAACCTGGCGGTGCGGACCTCTGTCTGTGTGTGTGTGTGTGTGTGT 224
Db 317 CAMCATCTACCTGTCTCAACCTGGCGGTAGCGGAGCTCTTCACTGTGAGCGTGTGTGT 376
Qy 225 CGT-----GCTGTCACTCCCTGGGAGAC---ACCTCAGACAGCGCGCTGTGTGTGTGT 275
Qy 377 CGTGGCCTGTGTCGCGCGCCCTGCGCCACTGCGCCCTTGGCTCCGTGTGTGTGTGTGTGT 436
Db 276 CCAGGGCATCTACCTGACCAACAGGTATACATGAGCATCAGCCTGTGTGTGTGTGTGTGT 335
Qy 437 GCTCAGCGTGTGAGCGGCTCAACATGTTTACCAGCGTCTTCTGTCTCACCGTGTGTGTGT 496
Db 336 GGAACGCTATGTGTGGCGGTGCGGACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 395
Qy 497 GGAACGCTACGTGTGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 556
Db 396 GGTGTGGCGCGGTGTGTGGCGGTCTCTGTGGTG 426

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Db 557 GGCCAGCTCATCAACCTGGCGTGTGGCTG 587

RESULT 4
US-10-750-185-61969
; Sequence 61969, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: NM11100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61969
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Bovine 19866880917942
; US-10-750-185-61969

Query Match          9.6%; Score 89; DB 7; Length 2095;
Best Local Similarity 47.9%; Pred. No. 5.3e-09;
Matches 402; Conservative 0; Mismatches 410; Indels 27; Gaps 4;

Qy 20 CCTGTGGCTCCAGCGACCTCACTGGCCCCCAGCGATCAAGCTGGGCTTCTACGGCTACT 79
Db 493 CCGTGTCTTCTGGCACCCGCCCTCTCCCATAGTCTGCGCTCTCTGGCGCAGTCT 552
Qy 80 TGGCGTCTCTGCTGGTGTAGCGCTGCTCAACAGCTGCGCTCTGGGGTGTCTGTCT 139
Db 553 TGGCGATGGAGTTGTCTCTGGGCTGTGGGGAACAGCTGGCTTCTCATCTTCTGCT 612
Qy 140 GCCGATGCAGTGGAGCGAGACCCGCATCTACATGACCAACCTGGCGGTGGCGGACC 199
Db 613 TGGCGACCGGCCCTTGGAGCTTCAACAGCTGTTCTGCTGAGCTGGTGGTGGCGACT 672
Qy 200 TCTGCTCTGTGCACTTGGCTTGTGCTGCACTCCCTGGGAGACACTCAGACACGC 259
Db 673 TCTCTCTGATCTCTCAACCTGGCCCTTCTGGTGGATTACTTCTTCCACGAGATCTGCG 732
Qy 260 -----CGTGTGCCAGCTCTCCAGGGATCTACTGACCAACAGTACATGA 307
Db 733 GCTTTGGGGACACCGCCTGCAAGTCAACCTGTTATGATGCCACCAACCGGACCA 792
Qy 308 GCATCAGCTGTGACGCGCATCGCGCTGGACCGCTATGTGCGCGTGGCGCAACCGCTGC 367
Db 793 GCGTGGTCTTCTCAGCGCGGTGGCGCTCAACCGTCTCTTGAAGTGGGTGGGCGCACACC 852
Qy 368 GTGCCCGGGGTGCGGTGCCCGAGCGGTGGCGCGCTGTGCGCGTCTCTGGGTGC 427
Db 853 ATGCGCTGACGAGCGCTCAGCTGGGGCGCTGCGCGGTGGCGCGGTCTCTGGG--- 909
Qy 428 TGGTCACTGGCTCTCTGGTGGTCTGCTGGGATTCAGAGGGCGGCTTCTGCT 487
Db 910 GGGCACTCTGCTCTCAACGGGCACTGCTCTGACCAACCACTCCAGCGGTCTTGGC 969
Qy 488 TCAG-----GAGCAGCGGCAATTTCACTCCATGCGGTTCCGCTGCTGGGAT 538
Db 970 TCAGTTACGAGTGGGCAAGAGACCTCGGCTCTCACTAGCTGGGACAGGCGCTTGTGG 1029
Qy 539 TCTACTGCGCTGCGCGGTGGTGTCTTCTGCTCCCTGAAGGTGTGACTGCGCTGGGCC 598
Db 1030 TGGTGAATCTTCTGCGCGTGGCGCTCATCTCTTTTGGCTGTGAGCATCAGCGCA 1089

RESULT 5
US-10-750-623-61969
; Sequence 61969, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: NM11100-1
; CURRENT APPLICATION NUMBER: US/10750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61969
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Bovine 19866880917942
; US-10-750-623-61969

Query Match          9.6%; Score 89; DB 7; Length 2095;
Best Local Similarity 47.9%; Pred. No. 5.3e-09;
Matches 402; Conservative 0; Mismatches 410; Indels 27; Gaps 4;

Qy 20 CCTGTGGCTCCAGCGACCTCACTGGCCCCCAGCGATCAAGCTGGGCTTCTACGGCTACT 79
Db 493 CCGTGTCTTCTGGCACCCGCCCTCTCCCATAGTCTGCGCTCTCTGGCGCAGTCT 552
Qy 80 TGGCGTCTCTGCTGGTGTAGCGCTGCTCAACAGCTGCGCTCTGGGGTGTCTGTCT 139
Db 553 TGGCGATGGAGTTGTCTCTGGGCTGTGGGGAACAGCTGGCTTCTCATCTTCTGCT 612
Qy 140 GCCGATGCAGTGGAGCGAGACCCGCATCTACATGACCAACCTGGCGGTGGCGGACC 199
Db 613 TGGCGACCGGCCCTTGGAGCTTCAACAGCTGTTCTGCTGAGCTGGTGGTGGCGACT 672
Qy 200 TCTGCTCTGTGCACTTGGCTTGTGCTGCACTCCCTGGGAGACACTCAGACACGC 259
Db 673 TCTCTCTGATCTCTCAACCTGGCCCTTCTGGTGGATTACTTCTTCCACGAGATCTGCG 732
Qy 260 -----CGTGTGCCAGCTCTCCAGGGATCTACTGACCAACAGTACATGA 307
Db 733 GCTTTGGGGACACCGCCTGCAAGTCAACCTGTTATGATGCCACCAACCGGACCA 792
Qy 308 GCATCAGCTGTGACGCGCATCGCGCTGGACCGCTATGTGCGCGTGGCGCAACCGCTGC 367
Db 793 GCGTGGTCTTCTCAGCGCGGTGGCGCTCAACCGTCTCTTGAAGTGGGTGGGCGCACACC 852
Qy 368 GTGCCCGGGGTGCGGTGCCCGAGCGGTGGCGCGCTGTGCGCGTCTCTGGGTGC 427
Db 853 ATGCGCTGACGAGCGCTCAGCTGGGGCGCTGCGCGGTGGCGCGGTCTCTGGG--- 909
Qy 428 TGGTCACTGGCTCTCTGGTGGTCTGCTGGGATTCAGAGGGCGGCTTCTGCT 487
Db 910 GGGCACTCTGCTCTCAACGGGCACTGCTCTGACCAACCACTCCAGCGGTCTTGGC 969
Qy 488 TCAG-----GAGCAGCGGCAATTTCACTCCATGCGGTTCCGCTGCTGGGAT 538
Db 970 TCAGTTACGAGTGGGCAAGAGACCTCGGCTCTCACTAGCTGGGACAGGCGCTTGTGG 1029
Qy 539 TCTACTGCGCTGCGCGGTGGTGTCTTCTGCTCCCTGAAGGTGTGACTGCGCTGGGCC 598
Db 1030 TGGTGAATCTTCTGCGCGTGGCGCTCATCTCTTTTGGCTGTGAGCATCAGCGCA 1089
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QY 537 ATTCTACTGCGCCCTGCGCGGTGGTCTTCTGCTCCCTGAAGCTGTGTGACTGCCCT 593
Db 853 GGTGGGCTTGGTGTGTACACTTCTCATGGGCTTCTGTGCGCCGTGCGGGCCAT 797

RESULT 8

US-10-750-623-36071/c
; Sequence 36071, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36071
; LENGTH: 1685
; TYPE: DNA
; ORGANISM: Bovine 19866880675545
US-10-750-623-36071

Query Match 9.5%; Score 88.2; DB 7; Length 1685;
Best Local Similarity 49.3%; Pred. No. 7.4e-09;
Matches 265; Conservative 0; Mismatches 263; Indels 9; Gaps 1;
QY 66 CTCTACGCCCTACTTGGGCGTCTGCTGGTGTAGGCGCTGTCTCAACAGCCTGGCGCT 125
Db 1333 CATCTCTTTCATCTACTCGTGGTGTGCTGGTGGGCTCTGTGGAACTCCATGGTCA 1274
QY 126 CTGGGTGTCTGTCGCCCATGACAGTGTGACGAGACCGGCATCTACATGACCAACT 185
Db 1273 CTACGTGATCTCTGCGCTACGCCAAGATGAAGACGCGCCACCAACATCTACATCTCAACCT 1214
QY 186 GCGGTGGCGACCTCTGCTGCTGTGACCTTGGCCCTTCTGCTGCTGCTCC----- 237
Db 1213 GGCATCGCCGATGAGCTGCTCATGCTCAGCGTGGCCCTTCTGCTGCTCCACATGCT 1154
QY 238 -CTCGGAGACACCTCAGACAGCGCGCTGTGCCAGCTCTCCAGGGCATCTACTGACCAA 296
Db 1153 TCGCCACTGGCCCTTTCGGCGCGCTACTCTGCCGCTCTGCTCAGCGTGGACGAGTCA 1094
QY 297 CAGGTACATGACATCAGCCTGGTCAACGGCCATCGCCGTGGACCGCTATGTGGCCGTGG 356
Db 1093 CATGTTACACGACATCTACTGTCTGCTGCTAGCGTGGACCGCTAGTGGCGGTGT 1034
QY 357 GCACCGGTGTGTCGGCGGCGTGGTCCCGAGGACGGTCCCGAGCGCGGTGTGCGCGGT 416
Db 1033 GCACCCCATCAAGGCGCGACGCTACCGCGCGCCACCGTGGCCAAAGTGGTGAATCTGGG 974
QY 417 CCTCTGGGTGCTGCTCATCGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 476
Db 973 CGTGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 914
QY 477 CGGCTTCTGCTTTCAGGAGCACCGGCAAAATTTCAACTCCATGCGGTTCOCGTGCTGGG 536
Db 913 CAACAGCGAGGACGCTGGCTGCAACATGCTCATGCGCGAGCCCGCCAGCGCTGGCT 854
QY 537 ATTCTACTGCGCCCTGCGGTGGTGTCTTCTGCTCCCTGAAGGTGGTGTGACTGCCCT 593
Db 853 GGTGGGCTTGGTGTGTACACTTCTCATGGGCTTCTGCTGCTGCTGCTGCTGCGGCGCAT 797

RESULT 9

US-11-127-877-29
; Sequence 29, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. P.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-29

Query Match 9.1%; Score 84.2; DB 11; Length 1077;
Best Local Similarity 49.3%; Pred. No. 4.3e-08;
Matches 311; Conservative 0; Mismatches 308; Indels 12; Gaps 3;
QY 82 GCGCTGCTGCTGGTGTAGGCTGCTGCTCAACAGCCTGGCGCTCTGGTGTCTGCTGCG 141
Db 181 GGAGCCATCTTCTGCGAGGGCTGTGCTCAACGGGCTGGCGCTGTACGTCTTCTGCTGC 240
QY 142 CGCATGACGAGTGTGAGGAGACCGCATCTACATGACAACTGGCGTGGCCGACCTC 201
Db 241 CGCACCCGGGCAAGACACCTCTAGTCACTACACCATCAACTGCTGTGTGACCATCTA 300
QY 202 TGCTGCTGTGCACCTTGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 261
Db 301 CTGGTAGGGCTGCTCCCTGCGCCACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 262 CTGTGCGAGCTCTCCAGGGATC---TACCTGACCAACAGGTACATGAGCATCAGCCTG 318
Db 361 CGCTGTGCTTCCCGCAGCTCTGCTGCTTCTTCTCAACATGCACTGCTCCATCTCTTTC 420
QY 319 CTCAGGCCATCGCGTGTGAGCGCTATGTCGCGTGGCGCACCGCTGCTGCTGCTGCTGCT 378
Db 421 CTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 379 CTGGGCTCCCGCAGGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 438
Db 481 TGCCCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 439 TCCCTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 498
Db 541 -----GTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 594
QY 499 CGGCACAATTTCACTCCATGCGGTTCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 558
Db 595 GCGCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 651
QY 559 GTGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 618
Db 652 CGCATCATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 711
QY 619 GCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 678
Db 712 CGGGCCATGACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 771
QY 679 GTGGTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 709
Db 772 CACGCCCGCAAGTGGCGCGTGGCGCTGTGGC 802

